

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2000, 10:25:11 ; Search time 3006.14 Seconds

(without alignments)
31.963 Million cell updates/sec

Title: US-09-202-455-6

Perfect score: 22

Sequence: 1 aagcccaagtcgtcgcac 22

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba1:*
2: gb_ba2:*
3: gb_cm:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sy:*
14: gb_un:*
15: em_fun:*
16: em_hum1:*
17: em_hum2:*
18: em_in:*
19: em_cm:*
20: em_or:*
21: em_ov:*
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24: em_pl:*
25: em_ro:*
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90: em_htg23:*
91: gb_pr6:*
92: gb_pr7:*
93: gb_sts1:*
94: gb_sts2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
C 1	22	100.0	754	12 AB032772	AB032772 Mus muscu
C 2	22	100.0	864	12 AB032771	AB032771 Mus muscu
C 3	22	100.0	951	12 AB008426	AB008426 Mus muscu
C 4	22	100.0	951	12 AB036798	AB036798 Mus muscu
C 5	22	100.0	2029	12 AB022036S4	AB022039 Mus muscu
C 6	22	100.0	2225	12 AF019048	AF019048 Mus muscu
C 7	22	100.0	2237	12 AF013170	AF013170 Mus muscu
C 8	22	100.0	2295	5 AR062119	AR062119 Sequence
C 9	22	100.0	2299	12 AF053713	AF053713 Mus muscu
C 10	18.8	85.5	930	9 AB037599	AB037599 Homo sapi
C 11	18.8	85.5	1823	11 AF013171	AF013171 Homo sapi
C 12	18.8	85.5	2201	11 AF019047	AF019047 Homo sapi

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c 13 18.8 85.5 2271 11 AF053712
c 14 18.8 85.5 113451 52 AC023297
c 15 18.8 85.5 205139 66 AL139382
c 16 17.2 78.2 3747 74 VTBGNTNR
c 17 17.2 78.2 147481 56 AC067762
c 18 17.2 78.2 160952 56 AC055711
c 19 17.2 78.2 168653 59 AC069241
c 20 17.2 78.2 169331 59 AC069430
c 21 17.2 78.2 183957 52 AC024224
c 22 17.2 78.2 209137 60 AC06510
c 23 17.2 78.2 230254 60 AC074163
c 24 17.2 78.2 247029 41 AC006514
c 25 16.8 76.4 39739 31 AC015123
c 26 16.8 76.4 251796 69 AL358788
c 27 16.8 76.4 300732 32 AE003450
c 28 16.4 74.5 15301 48 SPBC609
c 29 16.4 74.5 41037 42 AC017476
c 30 16.4 74.5 262131 32 AE003573
c 31 16.2 73.6 142 4 AF175474
c 32 16.2 73.6 142 4 AF175483
c 33 16.2 73.6 142 4 AF175484
c 34 16.2 73.6 142 4 AF175485
c 35 16.2 73.6 142 4 AF175487
c 36 16.2 73.6 142 4 AF175488
c 37 16.2 73.6 142 4 AF175489
c 38 16.2 73.6 142 4 AF175490
c 39 16.2 73.6 142 4 AF175492
c 40 16.2 73.6 143 4 AF175486
c 41 16.2 73.6 1058 12 AF053454
c 42 16.2 73.6 1086 1 AF013513
c 43 16.2 73.6 4269 91 AC017655
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ALIGNMENTS

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RESULT 1
AB032772/c 754 bp mRNA ROD 29-JUN-2000
LOCUS Mus musculus RANKL 3 mRNA for receptor activator of NF-kB ligand 3,
DEFINITION complete cds.
ACCESSION AB032772.1 GI:8843824
VERSION receptor activator of NF-kB ligand 3.
KEYWORDS Mus musculus CDNA to mRNA.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 864)
AUTHORS Ikeda,T., Takahashi,H. and Hirokawa,K.
TITLE Somatostatin, a new marker of osteoblast, regulates the expression
of RANKL isoforms
JOURNAL Unpublished (1999)
REFERENCE 2 (bases 1 to 754)
AUTHORS Ikeda,T.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru
Ikeda, School of Medicine, Tokyo Medical and Dental University,
Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,
Tokyo 113-8519, Japan (E-mail: tohru.ph2med.tmd.ac.jp,
Tel:81-3-5803-5176, Fax:81-3-5803-0123)
FEATURES
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/product="receptor activator of NF-kB ligand 3"

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RESULT 2
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LOCUS Mus musculus RANKL 2 mRNA for receptor activator of NF-kB ligand 2,
DEFINITION complete cds.
ACCESSION AB032771.1 GI:8843822
VERSION receptor activator of NF-kB ligand 2.
KEYWORDS Mus musculus CDNA to mRNA.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 864)
AUTHORS Ikeda,T.
TITLE Receptor activator of NF-kB ligand 2
JOURNAL Published Only in Database (2000) In press
REFERENCE 2 (bases 1 to 864)
AUTHORS Ikeda,T.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru
Ikeda, School of Medicine, Tokyo Medical and Dental University,
Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,
Tokyo 113-8519, Japan (E-mail: tohru.ph2med.tmd.ac.jp,
Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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QY 1 aagcccaaaagtagctgcgcatc 22
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Db 841 AAGCCCAAAAGTAGCTGCATC 820

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AB008426/c 951 bp mRNA ROD 02-MAY-1998
LOCUS Mus musculus mRNA for osteoclast differentiation factor (ODF),
DEFINITION complete cds.
AB008426
ACCESSION AB008426.1 GI:3041781
VERSION osteoclast differentiation factor (ODF).
KEYWORDS Mus musculus bone marrow stromal cells cell_line:ST2 CDNA to mRNA,
SOURCE clone_11b:pcdl-sra296 clone:pobm291.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 951)
AUTHORS Yasuda,H.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-1997) to the DDBJ/EMBL/GenBank databases.
Hinatake Yasuda, Snow Brand Milk Products Co., Ltd., Research
Institute of Life Science, 519 Shimo-Tsibashi, Ishidashi-machi,
Tochigi 329-05, Japan (E-mail:fvbd7042emb.infwed.or.jp,
Tel:0285-52-1331, Fax:0285-53-1314)
2 (sites)
REFERENCE Yasuda,H., Shima,N., Nakagawa,N., Yamaguchi,K., Kinoshita,M.,
AUTHORS Mochizuki,S., Tomoyasu,A., Yano,K., Goto,M., Murakami,A., Tsuda,E.,
Moriwaga,T., Higashio,K., Udagawa,N., Takahashi,N. and Suda,T.
TITLE Osteoclast differentiation factor is a ligand for
osteoprotegerin/osteoclastogenesis-inhibitory factor and is
identical to TRANCE/RANKL
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3597-3602 (1998)
MEDLINE 98188248
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Location/Qualifiers
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ICFRHETSGSVPTDYQLMAYVYVTSIKIPSSHNLMKGSGTKMWSGNSSEPHYSIN
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BASE COUNT 231 a 267 c 248 g 205 t
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Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

VERSION AB036798.1 GI:8843829
KEYWORDS RANKL 1.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 951)
AUTHORS Ikeda,T.
TITLE Published Only in Database (2000) In press
JOURNAL RANKL 1
REFERENCE 2 (bases 1 to 951)
AUTHORS Ikeda,T.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2000) to the DDBJ/EMBL/GenBank databases. Tohru
Ikeda, School of Medicine, Tokyo Medical and Dental University,
Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,
Tokyo 113-8519, Japan (E-mail:toru.pth@med.tmd.ac.jp,
Tel:81-3-5803-5176, Fax:81-3-5803-0123)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
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LOCUS AB022036S4 2029 bp DNA ROD 14-APR-2000
DEFINITION Mus musculus DNA for osteoclast differentiation factor, exon 5,
complete cds.
AB022039.1
VERSION AB022039.1 GI:4127268
KEYWORDS osteoclast differentiation factor.
SEGMENT 4 of 4
SOURCE Mus musculus (strain:129) embryonic stem cell DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Kodaira,K., Kodaira,K., Mizuno,A., Yasuda,H., Shima,N.,
Murakami,A., Ueda,M. and Higashio,K.
TITLE Cloning and characterization of the gene encoding mouse osteoclast
differentiation factor
JOURNAL Gene 230 (1), 121-127 (1999)
MEDLINE 99214075
REFERENCE 2 (bases 1 to 2029)
AUTHORS Kodaira,K.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1999) to the DDBJ/EMBL/GenBank databases.
Kunihiko Kodaira, YS New Technology Institute Inc., Molecular

Biology: Shimomishashi 519, Ishibashi-machi, Tochigi 329-0512,
Japan (E-mail:YENITE@net.or.jp, Tel:81-285-52-2821,
Fax:81-285-52-2824)

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Db 557 AAGCCCAAGTACTGCATC 536

RESULT 6
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LOCUS Mus musculus receptor activator of nuclear factor kappa B ligand
DEFINITION (RANKL) mRNA, complete cds.
ACCESSION AF019048
VERSION AF019048.1 GI:2612923
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
1 (bases 1 to 2225)
Anderson,D.M., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D. and
Tometsko,M.E., Galibert,L.
A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
Nature 390 (6656), 175-179 (1997)
98032977
2 (bases 1 to 2225)
Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E.,
Cosman,D., Dubose,R. and Galibert,L.
Direct Submission
Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA

FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 aagcccaagtagctgcac 22
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Db 1064 AAGCCCAAGTACTGCATC 1043

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AF013170/c 2237 bp mRNA ROD 05-NOV-1998
LOCUS Mus musculus TNF-related ligand TRANCE mRNA, complete cds.
DEFINITION AF013170
ACCESSION AF013170
VERSION AF013170.1 GI:2411497
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2237)
Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlicki,J., Chao,M.,
Kalachikov,S., Cayani,E., Bartlett,F.S. III, Frackel,W.N., Lee,S.Y.
and Choi,Y.
TRANCE is a novel ligand of the tumor necrosis factor receptor
family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)
97460112
2 (bases 1 to 2237)
Wong,B.R., Josien,R., Lee,S.Y., Sauter,B., Li,H.L., Steinman,R.M.
and Choi,Y.
TRANCE (tumor necrosis factor [TNF]-related activation-induced
cytokine), a new TNF family member predominantly expressed in T
cells, is a dendritic cell-specific survival factor
J. Exp. Med. 186 (12), 2075-2080 (1997)
98060869
3 (bases 1 to 2237)
Fuller,K., Wong,B., Fox,S., Choi,Y. and Chambers,T.J.
TRANCE is necessary and sufficient for osteoblast-mediated
activation of bone resorption in osteoclasts
J. Exp. Med. 188 (5), 997-1001 (1998)
98401035
4 (bases 1 to 2237)
Wong,B.R., Josien,R., Lee,S.Y., Vologodskaya,M., Steinman,R.M. and
Choi,Y.
The TRAF family of signal transducers mediates NF-kappaB activation
by the TRANCE receptor
J. Biol. Chem. 273 (43), 28355-28359 (1998)
98447691
5 (bases 1 to 2237)
Wong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.
Direct Submission
Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA

FEATURES
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BASE COUNT 636 a 470 c 519 g 612 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 22; DB 12; Length 2237;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1069 AAGCCCAAGATCGTCGATC 1048

RESULT 8

AR062119 2295 bp DNA PAT 29-SEP-1999
LOCUS AR062119
DEFINITION Sequence 6 from patent US 5843678.
ACCESSION AR062119
VERSION AR062119.1 GI:5989810
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2295)
AUTHORS Boyle,W.J.
TITLE Osteoprotegerin binding proteins
JOURNAL Patent: US 5843678-A 6 01-DEC-1998;
FEATURES
Source Location/Qualifiers
1..2295
BASE COUNT 648 a 487 c 538 g 622 t

BASE COUNT

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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aagccccaagatcgtcgatc 22
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Db 1085 AAGCCCAAGATCGTCGATC 1064

RESULT 9

AF053713 2299 bp mRNA ROD 09-MAY-1998
LOCUS AF053713
DEFINITION Mus musculus osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053713
VERSION AF053713.1 GI:3057147
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 2299)
Lacey,D.L., Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R.,
Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S.,
Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A.,
Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J.,

TITLE

Delaney,J. and Boyle,W.J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation

JOURNAL

Cell 93 (2), 165-176 (1998)

MEDLINE

98227661

REFERENCE

2 (bases 1 to 2299)

AUTHORS

Boyle,W.J.

TITLE

Direct Submission

JOURNAL

Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA

FEATURES

Location/Qualifiers

1..2299
/organism="Mus musculus"
/db_xref="taxon:10090"

CDS

/function="regulates osteoclast differentiation and
activation"
/codon_start=1
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/protein_id="AAC40113.1"
/db_xref="GI:3057148"

/translation="MRASRDYGYKLRSEEMSGPGVPHGEPHLPAPASAPAPPA
ASRSMFLALIGLGOVVCSTALFLYFRAOMDPRISDSSTCEFYRIIRLHENA
STLESEDLTPDSCRRMROFQAVOKELQHYGPORFSGAPAMGSMVDVQRKPE
AOPFAHLTINASTIPSGSHKVTLSWYHDROAKTSNMTLSNGKLRVNDGYYLYAN
ICFRHETSGSPYDYLQLMYVYVTSIKIPSHNLKMGSGSKMWSGNSSEPHYSIN
GGFKLRAGEEISIVSNPSLDPDQATYFGAFRVODID"

BASE COUNT 641 a 494 c 541 g 623 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 22; DB 12; Length 2299;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aagccccaagatcgtcgatc 22
|||||
Db 1097 AAGCCCAAGATCGTCGATC 1076

RESULT 10

AB037599 930 bp mRNA PRI 06-APR-2000
LOCUS AB037599
DEFINITION Homo sapiens mRNA for SODF/TRANCE, complete cds.
ACCESSION AB037599
VERSION AB037599.1 GI:6863047
KEYWORDS
SOURCE Homo sapiens male tongue epithelial-like squamous cell carcinoma
cell_line:SCC-4 CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (sites)
Nagai,M., Kyakumoto,S. and Sato,N.
Cancer cells responsible for humoral hypercalcemia express mRNA
encoding a secreted form of ODF/TRANCE that induces osteoclast
formation

JOURNAL

Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)

MEDLINE

20175237

REFERENCE

2 (bases 1 to 930)

AUTHORS

Nagai,M., Kyakumoto,S. and Sato,N.

TITLE

Direct Submission

JOURNAL

Submitted (26-JAN-2000) to the DDBJ/EMBL/Genbank databases.
Masazumi Nagai, Iwate Medical University School of Dentistry,
Department of Biochemistry, 19-1 Uchimaru, Morioka, Iwate 020-8505,
Japan (E-mail:imagai@iwate.med.ac.jp, Tel: +81-19-651-5111(ex.4436),
Fax: +81-19-654-4147)

FEATURES

Location/Qualifiers

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/db_xref="taxon:9606"
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/cell_type="epithelial-like squamous cell carcinoma"

gene /sex="male"
/tissue_type="tongue"
95..829
/gene="sodf/trance"
95..829
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/db_xref="GI:6863048"
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PSGSHKVSLSWYHDHNGKISNMTFSNKLIVNODGFYILPANCIFRHETSGDLA
EYLQIMVYTKTSIKIPSSHLMKGGSTKYMSGNSEPHFYSINVGGFRLRSGEISL
EVSNSPLDPPDADATYFGAFKVRDID"

BASE COUNT 283 a 184 c 200 g 260 t 3 others

ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 930;
Best Local Similarity 90.9%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aagccccaagtaagtcgcgc 22
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Db 806 AAGCCCAAGTATGTGCATC 785

RESULT 11
AF013171 1823 bp mRNA PRI 19-SEP-1997
LOCUS Homo sapiens TNF-related ligand TRANCE mRNA, partial cds.
DEFINITION AF013171
ACCESSION AF013171
VERSION AF013171.1 GI:2411499
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1823)
Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlinick,J., Chao,M.,
Kalachikov,S., Cayani,E., Bartlett,F.S. III, Frankel,W.N., Lee,S.Y.
and Choi,Y.
TRANCE is a novel ligand of the tumor necrosis factor receptor
family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)
JOURNAL 2 (bases 1 to 1823)
MEDLINE 97460112
REFERENCE Wong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.
Direct Submission
JOURNAL Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA

FEATURES
source
Location/Qualifiers
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EYLQIMVYTKTSIKIPSSHLMKGGSTKYMSGNSEPHFYSINVGGFRLRSGEIS
EVSNSPLDPPDADATYFGAFKVRDID"

BASE COUNT 569 a 305 c 380 g 569 t

ORIGIN

Query Match 85.5%; Score 18.8; DB 11; Length 1823;
Best Local Similarity 90.9%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aagccccaagtaagtcgcgc 22
|||||
Db 715 AAGCCCAAGTATGTGCATC 694

RESULT 12
AF019047 2201 bp mRNA PRI 22-NOV-1997
LOCUS Homo sapiens receptor activator of nuclear factor kappa B ligand
DEFINITION (RANKL) mRNA, complete cds.
ACCESSION AF019047
VERSION AF019047.1 GI:2612921
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2201)
Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
Tometsko,M.E., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D. and
Galibert,L.
A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
Nature 390 (6656), 175-179 (1997)
JOURNAL 98032977
REFERENCE 2 (bases 1 to 2201)
Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E.,
Cosman,D., Dubose,R. and Galibert,L.
Direct Submission
JOURNAL Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA

FEATURES
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Location/Qualifiers
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SRMFVALIGLGIVGVSALEPFYFRADOMPNRISDEGHCICIRILRLHENDFODI
TLESODTKLIPDSRRIKQAFQGVKELQIVGSOHRIAREKAVDSMDLAKRSKILAEQAFHILINADI
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EYLQIMVYTKTSIKIPSSHLMKGGSTKYMSGNSEPHFYSINVGGFRLRSGEISL
EVSNSPLDPPDADATYFGAFKVRDID"

BASE COUNT 658 a 429 c 497 g 617 t

ORIGIN

Query Match 85.5%; Score 18.8; DB 11; Length 2201;
Best Local Similarity 90.9%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aagccccaagtaagtcgcgc 22
|||||
Db 1059 AAGCCCAAGTATGTGCATC 1038

RESULT 13
AF053712/c 2271 bp mRNA PRI 09-MAY-1998
LOCUS Homo sapiens osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053712
VERSION AF053712.1 GI:3057145
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2271)
AUTHORS Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A.,
Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
Delaney, J. and Boyle, W.J.
TITLE Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
JOURNAL Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
REFERENCE 2 (bases 1 to 2271)
AUTHORS Boyle, W.J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA
FEATURES
source Location/Qualifiers
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EAPQPAHLINTIDIPSGSHKYSLSWYHDMGKAMTFSNGKLIYNODFFYLYA
NICERHHTSGDLATEYLOIMWYVTKSIKIPSSHTKMGSTKTKWSGNSSEHFEYSIN
VGGEFKLSGEISIEVSFSLDDPDQATYTGAKRVADIDP"
BASE COUNT 658 a 462 c 522 g 629 t
ORIGIN

AUTHORS
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L.,
Bouckgeater, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Chapel, V., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Deatellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,
Fenster, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heald, A., Horton, L.,
Howland, J., C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Landers, T., Larcocque, K., Lehoczy, J., Levine, R.,
Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
McKean, P., Mckern, A., McKernan, C., McPheters, R., Meldrum, J.,
Menais, L., Milova, T., Miranda, C., Mieng, V., Morrow, J., Naylor, J.,
Norman, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T., M.,
Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange, Thomas, N., Stojanovic, N.,
Subramanian, A., Talmas, J., Testave, S., Theodore, J., Tirelli, A.,
Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
Zody, M.
TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:1139552.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 1A020
Center clone name: 21.R.9
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 106493 bases at least Q40
Consensus quality: 109791 bases at least Q40
Consensus quality: 111178 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 112251; sum-of-contigs
Quality coverage: 3.5 in Q20 bases; agarose-fp
Quality coverage: 4.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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2264: contig of 2264 bp in length
2255 2364: gap of 100 bp
2355 6779: contig of 4415 bp in length
6730 6879: gap of 100 bp
11333 11432: contig of 4433 bp in length
11333 11432: gap of 100 bp
11433 17335: contig of 5903 bp in length
17336 17435: gap of 100 bp
17436 23308: contig of 5873 bp in length
23309 23408: gap of 100 bp
23409 28598: contig of 5190 bp in length
28599 28698: gap of 100 bp
28699 36183: contig of 7485 bp in length
36134 36283: gap of 100 bp
36234 44529: contig of 8246 bp in length
44530 44629: gap of 100 bp
44630 53672: contig of 9043 bp in length

* 53673 53772: gap of 100 bp
* 53773 62948: contig of 9176 bp in length
* 62949 63048: gap of 100 bp
* 63049 75673: contig of 12625 bp in length
* 75674 75773: gap of 100 bp
* 75774 92375: contig of 16602 bp in length
* 92376 92475: gap of 100 bp
* 92476 113451: contig of 20976 bp in length.
Location/Qualifiers
1. 113451

FEATURES

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2365. 6779
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6880. 11332
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11433. 17335
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17436. 23308
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36284. 44529
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44630. 53672
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53773. 62948
misc_feature
/note="assembly_fragment"
clone_end:SP6
vector_side:right"
63049. 75673
misc_feature
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75774. 92375
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ORIGIN

Query Match 85.5%; Score 18.8; DB 52; Length 113451;
Best Local Similarity 90.9%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aagcccaagacgacgcac 22
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DB 12283 AAGCCCAAGATGTCATC 12304

RESULT 15
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LOCUS AL139382/C
DEFINITION Homo sapiens chromosome 13 clone RP11-86N24, *** SEQUENCING IN
PROGRESS ***, 27 unordered pieces.
ACCESSION AL139382
VERSION AL139382.4 GI:8978069
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 205139)
AUTHORS Burton,J.
TITLE Direct Submission
JOURNAL Submitted (05-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,

COMMENT

CB10 1SA: UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequests@sanger.ac.uk
On Jul 7, 2000 this sequence version replaced gi:8386479.

Genome Center
Center: Sanger Centre
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

Project Information
Center project name: Ba86N24

Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: Plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 193731 bases at least Q40
Consensus quality: 198268 bases at least Q20
Insert size: 202539; sum-of-contigs
Insert size: 162413; 9.2% error; agarose-fp
Quality coverage: 3.08x in Q20 bases; sum-of-contigs Quality
coverage: 3.84x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 19231 19330: gap of 100 bp
* 19331 32371: contig of 13041 bp in length
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* 34971 42014: contig of 7044 bp in length
* 42015 42114: gap of 100 bp
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* 50154 50253: gap of 100 bp
* 50254 56692: contig of 6439 bp in length
* 56693 56792: gap of 100 bp
* 56793 61250: contig of 4458 bp in length
* 61251 61350: gap of 100 bp
* 61351 62561: contig of 1211 bp in length
* 62562 62661: gap of 100 bp
* 62662 75173: contig of 12512 bp in length
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* 75274 81438: contig of 6165 bp in length
* 81439 81538: gap of 100 bp
* 81539 87285: contig of 5747 bp in length
* 87286 87385: gap of 100 bp
* 87386 89590: contig of 2205 bp in length
* 89591 89690: gap of 100 bp
* 89691 91525: contig of 1835 bp in length
* 91526 91625: gap of 100 bp
* 91626 106940: contig of 15315 bp in length
* 106941 107040: gap of 100 bp
* 107041 115418: contig of 8378 bp in length
* 115419 115518: gap of 100 bp
* 115519 119162: contig of 3644 bp in length
* 119163 119262: gap of 100 bp
* 119263 121311: contig of 2049 bp in length
* 121312 121411: gap of 100 bp
* 121412 129170: contig of 7759 bp in length
* 129171 129270: gap of 100 bp
* 129271 141607: contig of 12337 bp in length
* 141608 141707: gap of 100 bp
* 141708 152435: contig of 10728 bp in length
* 152436 152535: gap of 100 bp
* 152536 158440: contig of 5905 bp in length
* 158441 158540: gap of 100 bp
* 158541 159553: contig of 1013 bp in length


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* 159554 159653: gap of 100 bp
* 159654 164333: contig of 4680 bp in length
* 164334 164433: gap of 100 bp
* 164434 182240: contig of 17807 bp in length
* 182241 182340: gap of 100 bp
* 182341 183761: contig of 1421 bp in length
* 183762 183861: gap of 100 bp in length
* 183862 188214: contig of 4353 bp in length
* 188215 188314: gap of 100 bp
* 188315 205139: contig of 16825 bp in length.
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32472. 34870
/note="assembly_fragment:00429"
fragment_chain:1"
34971. 42014
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42115. 50153
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fragment_chain:2"
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62662. 75173
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81539. 87285
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89691. 91525
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91626. 106940
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107041. 115418
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115519. 119162
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119263. 121311
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158541. 159553
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164434. 182240
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Best Local Similarity 90.9%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 135492 AAGCCCAAGTAGTGTGCATC 135471

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Search completed: November 1, 2000, 14:52:32
Job time: 16041 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OK nucleic - nucleic search, using sw model

Run on: November 1, 2000, 14:52:32 ; Search time 3006.14 Seconds
(without alignments)
29.058 Million cell updates/sec

Title: us-09-202-455-9

Perfect score: 20

Sequence: 1 atcagaagacagactact 20

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da1:*
2: gb_da2:*
3: gb_da3:*
4: gb_da4:*
5: gb_da5:*
6: gb_da6:*
7: gb_da7:*
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43: gb_da43:*

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2	20	100.0	754	12 AB032772	AB032772 Mus muscu
3	20	100.0	864	12 AB032771	AB032771 Mus muscu
4	20	100.0	951	12 AB008426	AB008426 Mus muscu
5	20	100.0	951	12 AB036798	AB036798 Mus muscu
6	20	100.0	2225	12 AF019048	AF019048 Mus muscu
7	20	100.0	2237	12 AF013170	AF013170 Mus muscu
8	20	100.0	2295	5 AR062119	AR062119 Sequence
9	20	100.0	2299	12 AF053713	AF053713 Mus muscu
10	18.4	92.0	66390	53 AC025129	AC025129 Homo sapi
11	18	90.0	182673	59 AC073105	AC073105 Homo sapi
12	18	90.0	186176	42 AC016994	AC016994 Homo sapi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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15 17.4 87.0 120515 91 HSJ744124
16 17.4 87.0 133925 9 AC004562
17 17.4 87.0 151578 70 AP001074
18 17.4 87.0 170992 70 AP001786
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20 17.4 87.0 174389 67 AL353598
21 17.4 87.0 175674 56 AC053465
22 17.4 87.0 176781 30 AC002989
23 17.4 87.0 177555 10 AC006450
24 17.4 87.0 179563 70 AP001521
25 17.4 87.0 179783 54 AC025988
26 17.4 87.0 193780 54 AC026004
27 17.4 87.0 225311 67 AL158052
28 17.4 87.0 323210 70 AP002397
29 17.4 87.0 332071 89 AP000905
30 17 85.0 148068 59 AC073067
31 17 85.0 188888 51 AC023051
32 17 85.0 189894 59 AC068656
33 17 85.0 194899 53 AC025763
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36 16.8 84.0 2201 11 AF019047
37 16.8 84.0 2271 12 AF053712
38 16.8 84.0 86380 12 NMU131017
39 16.8 84.0 99295 68 AL356673
40 16.8 84.0 127272 69 AL357973
41 16.8 84.0 141954 68 AL355480
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43 16.8 84.0 157848 43 AC018455
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45 16.8 84.0 160342 53 AC025492
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ALIGNMENTS

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RESULT 1
AB022036S2 468 bp DNA 14-APR-2000
LOCUS Mus musculus DNA for osteoclast differentiation factor, exon 2.
ACCESSION AB022037
VERSION AB022037.1 GI:4127266
KEYWORDS osteoclast differentiation factor.
SEGMENT 2 of 4
SOURCE Mus musculus (strain:129) male embryonic stem cell cell_line:E14
DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Kodaira,K., Kodaira,K., Mizuno,A., Yasuda,H., Shima,N.,
Muraikami,A., Ueda,M. and Higashio,K.
TITLE Cloning and characterization of the gene encoding mouse osteoclast
differentiation factor
JOURNAL Gene 230 (1), 121-127 (1999)
MEDLINE 99214075
REFERENCE 2 (bases 1 to 468)
AUTHORS Kodaira,K.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1999) to the DDBJ/EMBL/GenBank databases.
Kunihito Kodaira, YS New Technology Institute Inc., Molecular
Biology, Shimoiishibashi 519, Ishibashi-machi, Tochigi 329-0512,
Japan (E-mail:YISNET-net.or.jp, Tel:81-285-52-2821,
Fax:81-285-52-2824)
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FEATURES

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 186 ATCAGAGACGACTACT 205
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LOCUS Mus musculus RANKL 3 mRNA for receptor activator of NF-kB ligand 3,  
complete cds.  
DEFINITION AB032772  
ACCESSION AB032772  
VERSION AB032772.1 GI:8843824  
KEYWORDS Receptor activator of NF-kB ligand 3.  
SOURCE Mus musculus cDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (sites)  
AUTHORS Ikeda,T., Takahashi,H. and Hirokawa,K.  
TITLE Somatostatin, a new marker of osteoblast, regulates the expression  
of RANKL isoforms  
JOURNAL Unpublished (1999)  
REFERENCE 2 (bases 1 to 754)  
AUTHORS Ikeda,T.  
TITLE Direct Submission  
JOURNAL Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru  
Ikeda, School of Medicine, Tokyo Medical and Dental University,  
Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,  
Tokyo 113-8519, Japan (E-mail:toru.phn2med.tmd.ac.jp,  
Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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FEATURES

source

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atcagaagacagcactcact 20
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Db 240 ATCAGAGACAGCAGCCTACT 259

RESULT 6
AF019048 2225 bp mRNA ROD 22-NOV-1997
LOCUS Mus musculus receptor activator of nuclear factor kappa B ligand
DEFINITION (RANKL) mRNA, complete cds.
ACCESSION AF019048
VERSION AF019048.1 GI:2612923
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2225)
Anderson, D.M., Maraskovsky, E., Billingsley, W.L., Dougall, W.C.,
Tometsko, M.E., Roux, E.R., Teepe, M.C., Dubose, R.F., Cosman, D. and
Gallibert, L.
TITLE A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
JOURNAL Nature 390 (6565), 175-179 (1997)
MEDLINE 98032977
REFERENCE 2 (bases 1 to 2225)
Anderson, D.M., Billingsley, W., Dougall, W., Maraskovsky, E.,
Cosman, D., Dubose, R. and Gallibert, L.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA
FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atcagaagacagcactcact 20
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Db 376 ATCAGAGACAGCAGCCTACT 395

RESULT 7
AF013170 2237 bp mRNA ROD 05-NOV-1998
LOCUS Mus musculus TNF-related ligand TRANCE mRNA, complete cds.
DEFINITION AF013170
ACCESSION AF013170
VERSION AF013170.1 GI:2411497
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2237)
Wong, B.R., Rho, J., Arron, J., Robinson, E., Orlinick, J., Chao, M.,
Kalachikov, S., Cayani, E., Bartlett, F.S. III, Frankel, W.N., Lee, S.Y.
and Choi, Y.
TITLE TRANCE is a novel ligand of the tumor necrosis factor receptor
family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)
9/460112
2 (bases 1 to 2237)
Wong, B.R., Josten, R., Lee, S.Y., Sauter, B., Li, H.L., Steinman, R.M.
and Choi, Y.
TITLE TRANCE (tumor necrosis factor [TNF]-related activation-induced
cytokine), a new TNF family member predominantly expressed in T
cells, is a dendritic cell-specific survival factor
J. Exp. Med. 186 (12), 2075-2080 (1997)
98060869
3 (bases 1 to 2237)
Fuller, K., Wong, B., Fox, S., Choi, Y. and Chambers, T.J.
TITLE TRANCE is necessary and sufficient for osteoclast-mediated
activation of bone resorption in osteoclasts
J. Exp. Med. 188 (5), 997-1001 (1998)
98401035
4 (bases 1 to 2237)
Wong, B.R., Josten, R., Lee, S.Y., Vologodskaya, M., Steinman, R.M. and
Choi, Y.
TITLE The TNF family of signal transducers mediates NF-kappaB activation
by the TRANCE receptor
J. Biol. Chem. 273 (43), 28355-28359 (1998)
98447691.
5 (bases 1 to 2237)
Wong, B.R., Rho, J., Arron, J., Lee, S.Y., Robinson, E. and Choi, Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA
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 complete cds.
 ACCESSION AB032771
 VERSION AB032771.1 GI:8843822
 KEYWORDS receptor activator of NF-kB ligand 2.
 SOURCE Mus musculus CDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 864)
 AUTHORS Ikeda, T.
 TITLE Receptor activator of NF-kB ligand 2
 JOURNAL Published Only in Database (2000) In press
 REFERENCE 2 (bases 1 to 864)
 AUTHORS Ikeda, T.
 TITLE Direct Submission
 JOURNAL Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru
 Ikeda, School of Medicine, Tokyo Medical and Dental University,
 Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,
 Tokyo 113-8519, Japan (E-mail: toru.pth2med.tmd.ac.jp,
 Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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 complete cds.
 ACCESSION AB008426
 VERSION AB008426.1 GI:3041781
 KEYWORDS osteoclast differentiation factor (ODF).
 SOURCE Mus musculus bone marrow stromal cells cell_line:ST2 CDNA to mRNA,
 clone.lib:pCDL-SRa296 clone:pOBM291.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 951)
 AUTHORS Yasuda, H.
 TITLE Direct Submission
 JOURNAL Submitted (22-OCT-1997) to the DDBJ/EMBL/GenBank databases.
 Hisataka Yasuda, Snow Brand Milk Products Co., Ltd., Research
 Institute of Life Science, 519 Shimo-Ishibashi, Ishibashi-machi,
 Toohigi 329-05, Japan (E-mail: fvd07042emb.lifosce.or.jp,

REFERENCE 2 (sites)
 AUTHORS Yasuda, H., Shima, N., Nakagawa, N., Yamaguchi, K., Kinoshita, M.,
 Mochizuki, S., Tomoyasu, A., Yano, K., Goto, M., Murakami, A., Tsuda, E.,
 Morinaga, T., Higashio, K., Udagawa, N., Takahashi, N., and Suda, T.
 TITLE Osteoclast differentiation factor is a ligand for
 osteoprotegerin/osteoclastogenesis-inhibitory factor and is
 identical to TRANCE/RANKL
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3597-3602 (1998)
 MEDLINE 98188248
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 LOCUS AB036798
 DEFINITION Mus musculus mRNA for RANKL 1, complete cds.
 ACCESSION AB036798
 VERSION AB036798.1 GI:8843829
 KEYWORDS RANKL 1.
 SOURCE Mus musculus CDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 951)
 AUTHORS Ikeda, T.
 TITLE Direct Submission
 JOURNAL Submitted (11-JAN-2000) to the DDBJ/EMBL/GenBank databases. Tohru
 Ikeda, School of Medicine, Tokyo Medical and Dental University,
 Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,
 Tokyo 113-8519, Japan (E-mail: toru.pth2med.tmd.ac.jp,
 Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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BASE COUNT 636 a 470 c 519 g 612 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
AR062119 2295 bp DNA PAT 29-SEP-1998
SEQUENCE 6 from patent US 5843678.
ACCESSION AR062119
VERSION AR062119.1 GI:5989810
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2295)
AUTHORS Boyle, W.J.
TITLE Osteoprotegerin binding proteins
JOURNAL Patent: US 5843678-A 6 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..2295
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atcagaagacgactact 20
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Db 397 ATCAGAGACGACTACT 416

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DEFINITION Mus musculus osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053713
VERSION AF053713.1 GI:3057147
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2299)
AUTHORS Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A.,
Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
Delaney, J., and Boyle, W.J.
TITLE Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
JOURNAL Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
REFERENCE 2 (bases 1 to 2299)
AUTHORS Boyle, W.J.
JOURNAL Direct Submission
TITLE Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Angen Center Drive, Thousand Oaks, California 91320, USA

FEATURES

SOURCE
CDS

Location/Qualifiers
1..2299
/organism="Mus musculus"
/db_xref="taxon:10090"
170..1120
/function="regulates osteoclast differentiation and
activation"
/codon_start=1
/product="osteoprotegerin ligand"
/protein_id="AAC40113.1"
/db_xref="GI:3057148"
/translation="MRRASRDYGYLRSSEMGSGPVEHGPPLPAPAPAPPA
ASRSMFLAIGLIGGVASGLALFLYRAADPDRISDTHCYRILRLHKNGLD
STLESEDTLDCSRMKAOGAVOKELQHTVGPORSGAPAMMGSMVLAORGRPE
AQPFAHLITINASTIPSGSHVYTLSSRTHDRKMAKISMTLSNGKLRPNQDGFYLYAN
ICFRHETSGSVPTDYLQLMVYVVKTSIKIPSSNLMKGGSTKNWSGNSSEHFYSINV
GGFFKLAGEEISIOVSNPSLDDPDODATYFAGKAYODID"

BASE COUNT 641 a 494 c 541 g 623 t
ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 2299;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atcagaagacgactact 20
|||||
Db 409 ATCAGAGACGACTACT 428

RESULT 10
AC025129 66390 bp DNA HTG 21-MAR-2000
LOCUS Homo sapiens clone RP11-362B23, WORKING DRAFT SEQUENCE, 8 unordered
DEFINITION pieces.
ACCESSION AC025129
VERSION AC025129.2 GI:7272258
KEYWORDS HTG, HTGS_PHAISEL, HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 66390)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL Homo sapiens, clone RP11-362B23
REFERENCE 2 (bases 1 to 66390)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Bouhagalter, B., Brown, A., Burkett, G.,
Campoliano, A., Castle, A., Choe, P., Colangelo, M., Collins, S.,
Collumore, A., Cooke, P., Dearrellano, K., Dewar, R., Diaz, J.S.,
Dodgson, S., Domiano, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J., J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karakas, A.,
Klein, J., Labrecque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Lieuw, G., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPeckers, R.,
Meidirim, J., Menus, L., Minova, T., Miranda, C., Mlenka, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Tromann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tefaye, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J.,
Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, F.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
JOURNAL Direct Submission
COMMENT Submitted (05-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 21, 2000 this sequence version replaced g1:7158940.
All repeats were identified using RepeatMasker.

Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www.seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L7803

Center clone name: 362_B.23

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 62647 bases at least Q40

Consensus quality: 64420 bases at least Q30

Consensus quality: 65095 bases at least Q20

Insert size: 55000; agarose-fp

Insert size: 65690; sum-of-ctrls

Quality coverage: 4.8 in Q20 bases; agarose-fp

Quality coverage: 4.0 in Q20 bases; sum-of-ctrls

----- NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1204: contig of 1204 bp in length
 * 1205 1304: gap of 100 bp
 * 1305 3155: contig of 1851 bp in length
 * 3156 3255: gap of 100 bp
 * 3256 6760: contig of 3505 bp in length
 * 6761 6860: gap of 100 bp
 * 6861 9249: contig of 2389 bp in length
 * 9250 9349: gap of 100 bp
 * 9350 18770: contig of 9421 bp in length
 * 18771 18870: gap of 100 bp
 * 18871 29847: contig of 10977 bp in length
 * 29848 29947: gap of 100 bp
 * 29948 47118: contig of 17171 bp in length
 * 47119 47218: gap of 100 bp
 * 47219 66390: contig of 19172 bp in length.

FEATURES

source

1. 66390
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="RP11-362823"

/clone.lib="RPC1-11 Human Male BAC"

misc_feature

1. 1204
 /note="assembly-fragment"

misc_feature

1305. 3155
 /note="assembly-fragment"

misc_feature

3256. 6760
 /note="assembly-fragment"

misc_feature

6861. 9249
 /note="assembly-fragment"

misc_feature

/note="assembly-fragment"

misc_feature

clone_end:SP6
 vector_side:left"

misc_feature

9350. 18770
 /note="assembly-fragment"

misc_feature

18871. 29847
 /note="assembly-fragment"

misc_feature

29948. 47118
 /note="assembly-fragment"

misc_feature

47219. 66390
 /note="assembly-fragment"

BASE COUNT 17609 a 14210 c 15018 g 18846 t 707 others

Query Match 92.0%; Score 18.4; DB 53; Length 66390;
 Best Local Similarity 95.0%; Pred. No. 11;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0

1 atcagaagacagcactcact 20

Db 7233 ATCAGAGACAGCACTACT 7252

RESULT 11

AC073105/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

Project Information

Center project name: H.NH0464P18

Summary Statistics

Sequencing vector: M13; 100%

Chemistry: Dye-terminator Big Dye; 100% of reads

Chemistry: Dye-terminator Big Dye; 0% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 168154 bases at least Q40

Consensus quality: 172308 bases at least Q30

Consensus quality: 174249 bases at least Q20

Insert size: 178000; agarose-fp

Insert size: 179973; sum-of-ctrls

Quality coverage: 3.67 in Q20 bases; agarose-fp

Quality coverage: 3.72 in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1558: contig of 1558 bp in length

1559 1658: gap of unknown length

1659 3238: contig of 1580 bp in length

3239 3338: gap of unknown length

3339 6470: contig of 3132 bp in length

6471 6570: gap of unknown length

6571 9019: contig of 2449 bp in length

9020 9119: gap of unknown length

9120 11319: contig of 2200 bp in length

11320 11419: gap of unknown length

11420 14077: contig of 2658 bp in length

14078 14177: gap of unknown length

14178 17503: contig of 3326 bp in length


```
* 17504 17603: gap of unknown length
* 17604 21392: contig of 3789 bp in length
* 21393 21492: gap of unknown length
* 21493 24939: contig of 3447 bp in length
* 24940 25039: gap of unknown length
* 25040 29068: contig of 4029 bp in length
* 29069 33082: gap of unknown length
* 29169 33083 33182: contig of 3914 bp in length
* 33083 33183 36815: gap of unknown length
* 36815 36915: contig of 3633 bp in length
* 36916 42224: contig of 5309 bp in length
* 42225 42324: gap of unknown length
* 42325 47877: contig of 5553 bp in length
* 47878 47978: gap of unknown length
* 47978 52325: contig of 4348 bp in length
* 52326 52426 57081: gap of unknown length
* 52426 57082 57181: contig of 4656 bp in length
* 57082 57182 63081: gap of unknown length
* 57182 63082 63181: contig of 5900 bp in length
* 63082 63182 69925: gap of unknown length
* 63182 69926 70026: contig of 6744 bp in length
* 70026 79877: gap of unknown length
* 79877 79978 87549: contig of 9852 bp in length
* 79978 87549 87650: gap of unknown length
* 87550 87650 97089: contig of 7572 bp in length
* 87650 97089 97189: gap of unknown length
* 97090 105647: contig of 9440 bp in length
* 97189 105648 105748: gap of 8458 bp in length
* 105648 105748 115419: contig of unknown length
* 105748 115419 115519: gap of 9672 bp in length
* 115519 115520 124377: contig of unknown length
* 124377 124378 124478: gap of 8858 bp in length
* 124478 136660: contig of unknown length
* 136660 136761 151613: gap of 12183 bp in length
* 136761 151613 151713: contig of 14853 bp in length
* 151713 151714 165051: gap of unknown length
* 151714 165052 165152: contig of 13338 bp in length
* 165052 182673 182674: gap of unknown length
* 182673 182675: contig of 17522 bp in length.
```

FEATURES

SOURCE

```
1. 182673
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="Rp11-464P18"

misc_feature
/note="assembly_name:Contig4"
1. 1558
/note="assembly_name:Contig4"
1659. 3238
/note="assembly_name:Contig5"
3339. 6470
/note="assembly_name:Contig6"
6571. 9019
/note="assembly_name:Contig7"
9120. 11319
/note="assembly_name:Contig8"
11420. 14077
/note="assembly_name:Contig9"
14178. 17503
/note="assembly_name:Contig10"
clone_end:17
vector_side:left"

misc_feature
/note="assembly_name:Contig11"
17604. 21392
/note="assembly_name:Contig12"
21493. 24939
/note="assembly_name:Contig13"
25040. 29068
/note="assembly_name:Contig14"
29169. 33082
/note="assembly_name:Contig15"
33183. 36815
```

```
/note="assembly_name:Contig15"
clone_end:36
vector_side:right"
36916. 42224
/note="assembly_name:Contig16"
42325. 47877
/note="assembly_name:Contig17"
47978. 52325
/note="assembly_name:Contig18"
52426. 57081
/note="assembly_name:Contig19"
57182. 63081
/note="assembly_name:Contig20"
63182. 69925
/note="assembly_name:Contig21"
70026. 79877
/note="assembly_name:Contig22"
79978. 87549
/note="assembly_name:Contig23"
87650. 97089
/note="assembly_name:Contig24"
97190. 105647
/note="assembly_name:Contig25"
105748. 115419
/note="assembly_name:Contig26"
115520. 124377
/note="assembly_name:Contig27"
124478. 136660
/note="assembly_name:Contig28"
136761. 151613
/note="assembly_name:Contig29"
151714. 165051
/note="assembly_name:Contig30"
165152. 182673
/note="assembly_name:Contig31"
53616 a 35139 c 34992 g 56222 t 2704 others
```

Query Match 90.0%; Score 18; DB 59; Length 182673;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atcagaagacagcactca 18
|||||
DB 139699 ATCAGAGACAGCAGCCTCA 139682

```
RESULT 12
AC016994 AC016994 186176 bp DNA HTG 16-JUL-2000
LOCUS Homo sapiens chromosome 2 clone RP11-19U8, WORKING DRAFT SEQUENCE,
DEFINITION 16 unordered pieces.
ACCESSION AC016994.5 GI:9230814
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 186176)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 186176)
TITLE Direct Submission
AUTHORS Submitted (09-DEC-1999) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jul 16, 2000 this sequence version replaced gi:8569724.
----- Genome Center -----
```

```

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0019508
----- Summary Statistics -----
Sequencing vector: M13, 71%
Sequencing vector: Plasmid, 29%
Chemistry: Dye-primer RT; 71% of reads
Chemistry: Dye-terminator Big Dye, 29% of reads
Assembly program: Phrap; version 0.99019
Consensus quality: 177898 bases at least Q40
Consensus quality: 180830 bases at least Q30
Consensus quality: 182406 bases at least Q20
Insert size: 187000; agarose-fp
Insert size: 184676; sum-of-ctngs
Quality coverage: 6.89 in Q20 bases; agarose-fp
Quality coverage: 6.04 in Q20 bases; sum-of-ctngs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1389: contig of 1389 bp in length
* 1390 1489: gap of unknown length
* 1490 2756: contig of 1267 bp in length
* 2757 2836: gap of unknown length
* 2857 4074: contig of 1218 bp in length
* 4075 4174: gap of unknown length
* 4175 5443: contig of 1269 bp in length
* 5444 5543: gap of unknown length
* 5544 6701: contig of 1158 bp in length
* 6702 6801: gap of unknown length
* 6802 8009: contig of 1208 bp in length
* 8010 8109: gap of unknown length
* 8110 9195: contig of 1086 bp in length
* 9196 9295: gap of unknown length
* 9296 10487: contig of 1192 bp in length
* 10488 10587: gap of unknown length
* 10588 12117: contig of 1530 bp in length
* 12118 12217: gap of unknown length
* 12218 13331: contig of 1114 bp in length
* 13332 13431: gap of unknown length
* 13432 15095: contig of 1664 bp in length
* 15096 15195: gap of unknown length
* 15196 17531: contig of 2336 bp in length
* 17532 17631: gap of unknown length
* 17632 20585: contig of 2864 bp in length
* 20596 20695: gap of unknown length
* 20696 39643: contig of 18948 bp in length
* 39743 39743: gap of unknown length
* 39744 86154: contig of 46411 bp in length
* 86155 86254: gap of unknown length
* 86255 186176: contig of 99922 bp in length.
*
* Location/Qualifiers
* 1. .186176
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="2"
* /clone="RP11-19308"
* 1. .1389
* /note="assembly_name:Contig11"
* 1490. .2756
* /note="assembly_name:Contig22"
* 2857. .4074
* /note="assembly_name:Contig27"
* 4175. .5443
* /note="assembly_name:Contig28"
* 5544. .6701

```

```

misc_feature /note="assembly_name:Contig29" .6802. .8009
/note="assembly_name:Contig30"
8110. .9195
misc_feature /note="assembly_name:Contig31"
.9296. .10487
/note="assembly_name:Contig32"
10588. .12117
misc_feature /note="assembly_name:Contig33"
12218. .13331
/note="assembly_name:Contig35"
13452. .15095
misc_feature /note="assembly_name:Contig37"
15196. .17531
/note="assembly_name:Contig38"
17632. .20595
misc_feature /note="assembly_name:Contig39"
20696. .39643
/note="assembly_name:Contig40
clone_end:SP6
vector_side:right"
misc_feature /note="assembly_name:Contig41
clone_end:R7
vector_side:left"
misc_feature /note="assembly_name:Contig42"
86255. .186176
/note="assembly_name:Contig43"
37022 c 37474 g 54612 t 1505 others

BASE COUNT 55563 n 37022 c 37474 g 54612 t 1505 others
ORIGIN

Query Match 90.0%; Score 18; DB 42; Length 186176;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

oy 1 atcagaagacagcactca 18
|||||
Db 50029 ATCAGACAGCAGCACTCA 50046

RESULT 13
AC005040/c AC005040 bp DNA PRI 21-DEC-1999
LOCUS Homo sapiens BAC clone RP11-519H15 from 2, complete sequence.
DEFINITION AC005040
AC005040
AC005040.2 GI:4508119
VERSION HTG.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 189949)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792.
REFERENCE 2 (bases 1 to 189949)
AUTHORS Madsen, C., Bauer, C. and Eldred, J.
TITLE The sequence of Homo sapiens BAC clone RP11-519H15
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 189949)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis
MO 63108, USA
REFERENCE 4 (bases 1 to 189949)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis
MO 63108, USA
REFERENCE 5 (bases 1 to 189949)

```



```

repeat_region      /rpt_family="Alu"
                    28329..28598
misc_feature        /rpt_family="MER89"
                    28602..28663
                    /note="match to EST AA210926 (MID:g1809598) zq89g07.r1"
repeat_region      /rpt_family="Alu"
                    29312..29618
repeat_region      /rpt_family="Alu"
                    29908..30308
repeat_region      /rpt_family="MALR"
                    30504..30828
repeat_region      /rpt_family="MER1_type"
                    30829..31552
repeat_region      /rpt_family="MER2_type"
                    31553..31574
repeat_region      /rpt_family="MER1_type"
                    31675..31784
repeat_region      /rpt_family="Alu"
                    32887..32897
repeat_region      /rpt_family="AT_rich"
                    32898..33305
repeat_region      /rpt_family="Alu"
                    33032..33457
                    /db_xref="GI:1233247"
STS

```

```

Query Match      90.0%; Score 18; DB 9; Length 189949;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 atcagaagacagactca 18
    |||||
Db 30037 ATCAGAAGACAGACTCA 30020

RESULT 14
AR062114      52 bp      DNA      PAT      29-SEP-1999
LOCUS          AR062114
DEFINITION     Sequence 1 from patent US 5843678.
ACCESSION      AR062114
VERSION        AR062114.1 GI:589805
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 52)
AUTHORS       Boyle,M.J.
TITLE         Osteoprotegerin binding proteins
JOURNAL       Patent: US 5843678-A 1 01-DEC-1998;
FEATURES       Location/Qualifiers
                source          1..52
                /organism="unknown"
BASE COUNT     13 a      15 c      8 g      16 t
ORIGIN

```

```

Query Match      87.0%; Score 17.4; DB 5; Length 52;
Best Local Similarity 94.7%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2 tcagaagacagactact 20
    |||||
Db 30 TCTGAGACAGACACTACT 48

RESULT 15
HSJ744124
LOCUS          HSJ744124
DEFINITION     Human DNA sequence from clone RP4-744124 on chromosome 6p12.1-21.2
                Contains a novel gene (KIA0646 (new zinc finger protein)), part of
                a novel gene (similar to a novel human gene mapping to chromosome
                22q13.3 similar to yeast ORF YOR070C, putative GTPase Activator),
                ESTs, STSS, GSSs and a CpG Island, complete sequence.
ACCESSION      AL096712
VERSION        AL096712.20 GI:6425593

```

KEYWORDS
SOURCE human
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 120515)
TITLE Direct Submission
JOURNAL Tracey,A.
Submitted (18-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA. UK. E-mail enquiries: humquey@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Nov 15, 1999 this sequence version replaced gi:6273550.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

COMMENT

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TRERBL; Wp., WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/C.elegans/wormpep> RP4-744124 is from the library RPCI-4 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR:PCYRAC2>

FEATURES

```

source          Location/Qualifiers
1..120515
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP4-744124"
/clone_lib="RPCI-4"
/map="p12.1-21.2"
1..379
/note="LIPB3 repeat: matches 5766..6145 of consensus"
complement(501..890)
/note="match: GSS: Em:B65724"
complement(519..890)
/note="match: GSS: Em:A0066699"
529..890
/note="match: GSS: Em:B41075"
complement(593..890)
/note="match: GSS: Em:AQ766846"
600..890
/note="match: GSS: Em:A0109548"
613..890
/note="match: GSS: Em:A0066878"
complement(643..890)
/note="match: STS: Em:AA937116"
891..1144
/note="UTR4 repeat: matches 332..588 of consensus"
1378..1712
/note="MER2 repeat: matches 2..345 of consensus"
1737..2257
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2462..2502
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2549..2610
repeat_region

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4148..4347
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4365..4399
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4483..4874
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5815..5967
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5972..6247
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7974..8338
repeat_region /note="match: STS: Em:R51865"
7974..8230
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LVINDINKKVNINSSVEKERRIYLIRERKRLFL"
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12882..13487
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13744..14023
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14049..14824
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14941..15030
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15051..15317
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16559..16836
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17039..17346
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24063..24373
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Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 26200 ATCAGAGACGACCTCACC 26218
Search completed: November 1, 2000, 14:52:50
Job time: 16059 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2000, 14:55:35 ; Search time 141.28 Seconds
(without alignments)
793.247 Million cell updates/sec

Title: US-09-202-455-19

Perfect score: 741
Sequence: 1 ggcagatgacccataag.....aagtcgagatagattga 741

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Checked: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Issued_Patents.NA.*
- 2: /cgn2.6/ptodata/1/ina/5A.COMB.seq.*
- 3: /cgn2.6/ptodata/1/ina/5B.COMB.seq.*
- 4: /cgn2.6/ptodata/1/ina/5C.COMB.seq.*
- 5: /cgn2.6/ptodata/1/ina/5D.COMB.seq.*
- 6: /cgn2.6/ptodata/1/ina/6.COMB.seq.*
- 7: /cgn2.6/ptodata/1/ina/Backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	741	100.0	954	US-08-996-139-12	Sequence 12, Appl
2	522.2	70.5	1630	US-08-996-139-10	Sequence 10, Appl
3	520.6	70.3	2295	US-08-842-842-6	Sequence 6, Appl
4	69.4	9.4	1042	US-08-584-031-2	Sequence 2, Appl
5	69.4	9.4	1042	US-08-780-496-2	Sequence 2, Appl
6	69.4	9.4	1521	US-08-670-354-3	Sequence 3, Appl
7	69.4	9.4	1521	PCT-US96-10895-3	Sequence 3, Appl
8	69.4	9.4	1751	US-08-670-354-1	Sequence 1, Appl
9	69.4	9.4	1751	PCT-US96-10895-1	Sequence 1, Appl
10	57.6	7.8	1366	US-08-670-354-5	Sequence 5, Appl
11	57.6	7.8	1366	PCT-US96-10895-5	Sequence 5, Appl
12	37.4	5.0	390	US-08-584-031-3	Sequence 3, Appl
13	37.4	5.0	390	US-08-780-496-3	Sequence 3, Appl
14	37.4	5.0	7218	US-08-232-463-14	Sequence 14, Appl
15	35.6	4.8	59	US-08-842-842-5	Sequence 5, Appl
16	32.4	4.4	3095	5231168-1	Patent No. 5231168
17	30.6	4.1	2152	US-08-338-543-1	Sequence 1, Appl
18	30.6	4.1	3126	US-08-929-329-2	Sequence 2, Appl
19	30.6	4.1	3139	US-07-894-212A-1	Sequence 1, Appl
20	30.2	4.1	8387	US-08-532-814-1	Sequence 1, Appl
21	30.2	4.1	43795	US-08-742-185-101	Sequence 101, Appl
22	29.8	4.0	1440	US-08-836-022A-10	Sequence 10, Appl
23	29.8	4.0	1440	US-08-743-637B-174	Sequence 174, Appl
24	29.8	4.0	1440	US-08-526-840B-174	Sequence 174, Appl
25	29.2	3.9	3732	US-09-212-971-7	Sequence 7, Appl
26	29	3.9	591	US-08-788-954-1	Sequence 1, Appl

27	29	3.9	1374	1	US-08-093-372-3	Sequence 3, Appl
28	28.8	3.9	279	1	US-08-186-222-3	Sequence 3, Appl
29	28.8	3.9	1282	1	US-08-361-920-22	Sequence 22, Appl
30	28.8	3.9	1282	1	US-08-479-939-22	Sequence 22, Appl
31	28.8	3.9	1282	2	US-08-483-432-22	Sequence 22, Appl
32	28.8	3.9	1519	1	US-08-090-523-9	Sequence 9, Appl
33	28.8	3.9	1519	1	US-08-398-627-9	Sequence 9, Appl
34	28.8	3.9	1519	1	US-08-406-858-9	Sequence 9, Appl
35	28.8	3.9	1519	6	PCT-US91-04036-9	Sequence 9, Appl
36	28.8	3.9	1519	6	PCT-US94-05275-9	Sequence 9, Appl
37	28.8	3.9	1823	1	US-08-145-995A-1	Sequence 1, Appl
38	28.8	3.9	1823	2	US-08-451-747-1	Sequence 1, Appl
39	28.8	3.9	2730	2	US-08-339-129-1	Sequence 1, Appl
40	28.6	3.9	2417	1	US-08-011-358B-1	Sequence 1, Appl
41	28.6	3.9	2417	2	US-08-464-051-1	Sequence 1, Appl
42	28.6	3.9	2417	2	US-08-464-051-1	Sequence 1, Appl
43	28.6	3.9	2417	5	US-08-554-385-2	Sequence 2, Appl
44	28.6	3.9	9890	1	US-08-232-463-18	Sequence 18, Appl
45	28.4	3.8	52	3	US-08-842-842-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-12
; Sequence 12, Application US/08996139
; Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOC# NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

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?      ?    HYPOTHEITICAL: NO  
?      ?    ANTI-SENSE:   NO  
?      ?    ORIGINAL SOURCE:  
?      ?    ORGANISM: Homo sapiens  
?      ?    IMMEDIATE SOURCE:  
?      ?     LIBRARY:  
?      ?    CLONE: huraNKL (full length)  
?      ?    FEATURE:  
?      ?    NAME/KEY: CDS  
?      ?    LOCATION: 1..951  
US-08-996-139-12
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OY	61	agactccatgaaaaatgycagattttcaagaacacaactctggaagtgcaagaatacaaaatla	120
Dp	274	AGACTCCATGAATAATGCAGATTTTCAAGACACAACTCTGGAGATCAAGATACAAAATTA	333
OY	121	atacctgattcaatgtaagagaattaacaaggccttcaaggagctgtgcaaaagaaatla	180
Dp	334	ATACCTGGATTTATGTAGAGAAATTAACAGCGCTTTCAAGAGAGCTGTGCAAAAGAAATTA	393
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Dp	394	CAACATATCGTTGGATCCACACATATCAGACAGAAAGCGATGGATGGCTCATGG	453
OY	241	ttagatctgagcaagaaggagaagacttgaagctcgaagccttctgtcatactcaattaat	300
Dp	454	TTAGATCTGGCCAAAGAGAGACGTAAGCTGAGGCTTGTGCTATGCATCATTAAT	513
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Dp	514	GCCACCGACATCCCATCTGGTTCCTCAATAAAGTGAGTGTGCTTGGTACCATGATCGG	573
OY	361	ggttggagccaagatctccaacatgacttttgaatgaaatgaaacatagtaataatcagat	420
Dp	574	GTTTGGGCCAAGATCTCCAAATATACTTTATGCAATGAGAAACTAATATATTAATCAGAT	633
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Dp	634	GGCTTTATATACGTGTAAGCCAACTATTGCTTGCATCATGAAACTTCAAGAGACCTA	693
OY	481	gctacagagatcttccaactaaatggtgtaagtcactaaacacagcatcaaatcccaagt	540
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RESULT 2
US-08-996-139-10
; Sequence 10, Application US/08996139

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1 Patent No.65017729
2 GENERAL INFORMATION:
3 APPLICANT: Anderson, Dirk M.
4 APPLICANT: Galibert, Laurent
5 APPLICANT: Maraskovsky, Eugene
6 TITLE OF INVENTION: Receptor Activator of NF-kappaB
7 NUMBER OF SEQUENCES: 19
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Immunex Corporation, Law Department
10 STREET: 51 University Street
11 CITY: Seattle
12 STATE: WA
13 COUNTRY: USA
14 ZIP: 98101
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: Apple Power Macintosh
18 OPERATING SYSTEM: Apple Operating System 7.5.5
19 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/996,139
22 FILING DATE: 22 DECEMBER 1997
23 CLASSIFICATION:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: USSN 60/064,671
26 FILING DATE: 14 OCTOBER 1997
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: USSN 08/813,509
29 FILING DATE: 07 MARCH 1997
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: USSN 08/772,330
32 FILING DATE: 23 DECEMBER 1996
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Perkins, Patricia Anne
35 REGISTRATION NUMBER: 34,693
36 REFERENCE/DOCKET NUMBER: 2551-A
37 TELECOMMUNICATION INFORMATION:
38 TELEPHONE: (206)587-0430
39 TELEFAX: (206)233-0644
40 INFORMATION FOR SEQ ID NO: 10:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 1630 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46 MOLECULE TYPE: cDNA
47 HYPOTHETICAL: NO
48 ANTI-SENSE: NO
49 ORIGINAL SOURCE:
50 ORGANISM: Mus musculus
51 IMMEDIATE SOURCE:
52 LIBRARY:
53 CLONE: RANKL
54 FEATURE:
55 NAME/KEY: CDS
56 LOCATION: 3..884
57 US-08-996-139-10

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Best Local Similarity 82.6%; Pred. No. 3,9e161;
Matches 612; Conservative 0; Mismatches 122; Indels 6; Gaps 1

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Oy 61 agaccctgtgnaatggcagatttccaagaacaaactctggagatgcagaataaatta 120
Db 213 AGACTTCATGAAAAGCGCAGATTTCAGAGACTCGACTCTGGAAATGGAACAC-----A 266
Oy 121 atactgattatctgtaggaagaattaaacagagccttccaagagcctgtgcnaaaggaa 180

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Db	267	CTACCTGCATCTCCTCAGAGAGATGAACAAGACCTTTTCAGGGGGGGCCGTCAGAAAGSAATG	326
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Db	327	CAACACATTGTGGGGCCCAACACCGCTTTTCAGGAGCTCCACCTAATGATGGAAGGCTCATGG	386
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Db	387	TTGATGTGGCCCAAGCGAGGCAACCTCGAGGCCAGCATTTTGACACCTCACCACCTAAT	446
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Db	627	CCTACAGACTATCTTCACCTATGTGTATGCTTTAAACACACATCAAAAATCCCAAGT	686
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Db	747	TTTTATTCATAAATGTGGGGGATTTTTCACGCTCCGAGCTGCTGAAGAAATTAAGCAT	806
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Db	807	CAGGTCACAACTCTCTCTCTGATCCGATCAAGATGCGACGTACTTTGGGGCTTTC	866
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<p>RESULT 3 US-08-842-842-6 Sequence 6, Application US/08842842 Patent No. 5843678</p> <p>GENERAL INFORMATION: APPLICANT: Boyle, William J. TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: ADDRESSEE: Amgen, Inc. STREET: 1840 Dehavenland Drive CITY: Thousand Oaks STATE: California COUNTRY: USA ZIP: 91230-1789</p> <p>COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/842,842 FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B. REFERENCE/DOCKET NUMBER: A-451 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 2295 base pairs</p>			

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: TYPE: nucleic acid
: STRANDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 158..1105
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US-08-842-842-6

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Db	548	CAACACATTTGIGGGGCCACAGCGGCTTCTCAGAGAGTCCACGATATGATGGAAGGCTCATGG	607
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Db	608	TTGGATGTGGGCCCGACGAGGCAAGCCCTGAAGGCCACCAATTTGACACCTCCACATCATAT	667
OY	301	gccaccgacaccccatctgtgttcccaaaaagttagctctctccctcttgatcatatcgtg	360
Db	668	GCTGCGACGATCCCATGGGTTCCCATTAAGTCACTCTGTCTCTTGTTGATCCACGATGCA	727
OY	361	ggttgggccaagatctccaacatgacttttagcaatgaaaaactaatagtaatacagat	420
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OY	421	ggctttatttcccgatatgcacaatttgtttcgacatcatgaaacttcaggagaccta	480
Db	788	GGCTTCAATTACCGTACGGCCAACTTTGGCTTGGCATCATGTAAACATCGGGAACCGTA	847
OY	481	gctacagagtacttccaactaatggtgtacgtctactaaacaacagcatcaaaaatcccaagt	540
Db	848	CCTACAGACTCTCTTCAAGCTGATGGTATATGTGTTAAACCGACATCAAAATCCCAAGT	907
OY	541	tctcataccctgatgaaagaggaagcaccaaatattgtgtcaggagaaatcttgaatccat	600
Db	908	TCTCATTAACCTGATGAAGAAAGGGAGACACAAAACATGTGCGGGCAATCTGATATCCAC	967
OY	601	ttttattcccaaaacgtttgtgtaatttttaagtctcgtctgagaagaatccagcac	660
Db	968	TTTTATTCCATAAATGTTGGGGGATTTTAAACCTCCGAGCTGTTGAAGAATAATAGCAT	1027
OY	661	gaggtctccajccctccctacttgatgacgcgaatcagaatgcaacatactttggggcttt	720
Db	1028	CAGGATGCCAACCCTTCCGCTGGATCGGATCAAGATCGACGTAATTTGGGGGCTTTC	1088
OY	721	aaagtgcagatataagattga 741	
Db	1088	AAAGTTCAGGACATAGACTGA 1108	

RESULT 4
US-08-584-031-2
: Sequence 2, Application US/08584031A
: Patent No. 6030945.
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.

NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: HuAIC-dv
FEATURE:
NAME/KEY: CDS
LOCATION: 78..383
US-08-670-354-3

Query Match 9.4%; Score 69.4; DB 2; Length 1521;
Best Local Similarity 51.9%; Pred. No. 4.6e-13;
Matches 182; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

QY 378 caacatgacttttaagcaagaaactaagtaacaggaagcttttaactgta 437
DB 424 CAACCTTGCACTTGAGGAAAGTGAGTGTGCTCATCGAATAAGGTTTACTACATCTA 483
QY 438 tgcacaacttcttcgcacatcatgaacttcagagacctagctacagagatctca 497
DB 484 TTCCCAACATACTTTCGATTTTCAGAGAGAAATAAAGA---AAACACAAGAAGACACA 540
QY 498 actaatggtgtacgtactcaaaacagcatcaaatcccaagttctcaacctgatga 557
DB 541 ACAAAAGGTCATATATTTTACAAATACACAAGTTATCCTGACCCTATATTTGTGATGAA 600
QY 558 agagagaagcaccagaatgtgtcagaggaatctgaattccattttattccataagct 617
DB 601 AAGTGCTAGAAATAGTGTGTTGGTCTTAAGATGCAAGATATGACTATATTCATCTATCA 660
QY 618 tggtagatttttaagttacggtctgagaggaatcagcatcagagctcacaaccctc 677
DB 661 AGGGGGAATATTGAGCTTAAGGAAATGACAGAAATTTTGTTCGTAAACAATAGACA 720
QY 678 cttaactggtcggatcagagatgacaatacttggggcttttaagttcg 728
DB 721 CTGTATAGACATGACCATGAAACCGAGTTTTCGGGGCCTTTTATGTTGG 771

RESULT 7
PCT-US96-10895-3
Sequence 3, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: HuAIC-dv
FEATURE:
NAME/KEY: CDS
LOCATION: 78..383
PCT-US96-10895-3

Query Match 9.4%; Score 69.4; DB 6; Length 1521;
Best Local Similarity 51.9%; Pred. No. 4.6e-13;
Matches 182; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

QY 378 caacatgacttttaagcaagaaactaagtaacaggaagcttttaactgta 437
DB 424 CAACCTTGCACTTGAGGAAAGTGAGTGTGCTCATCGAATAAGGTTTACTACATCTA 483
QY 438 tgcacaacttcttcgcacatcatgaacttcagagacctagctacagagatctca 497
DB 484 TTCCCAACATACTTTCGATTTTCAGAGAGAAATAAAGA---AAACACAAGAAGACACA 540
QY 498 actaatggtgtacgtactcaaaacagcatcaaatcccaagttctcaacctgatga 557
DB 541 ACAAAAGGTCATATATTTTACAAATACACAAGTTATCCTGACCCTATATTTGTGATGAA 600
QY 558 agagagaagcaccagaatgtgtcagaggaatctgaattccattttattccataagct 617
DB 601 AAGTGCTAGAAATAGTGTGTTGGTCTTAAGATGCAAGATATGACTATATTCATCTATCA 660
QY 618 tggtagatttttaagttacggtctgagaggaatcagcatcagagctcacaaccctc 677
DB 661 AGGGGGAATATTGAGCTTAAGGAAATGACAGAAATTTTGTTCGTAAACAATAGACA 720
QY 678 cttaactggtcggatcagagatgacaatacttggggcttttaagttcg 728
DB 721 CTGTATAGACATGACCATGAAACCGAGTTTTCGGGGCCTTTTATGTTGG 771

RESULT 8
US-08-670-354-1
Sequence 1, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis

QY 438 actaatggtacgtcactcaaaacacgacatcaaaatcccaagttctcatccctgatgaa 557
 Db 699 ACAATGCTCCATATATATTAACAATAACAGATATCTGACCCCTATATTTGATGAA 758
 QY 558 agggagagcccaagttatggtcaggaattctgaattccatttttttcataaagt 617
 Db 759 AAGTCTGAATAATGTTGTGCTTAAGATGCAAGATATGAGACTCTATTCATCTATCA 818
 QY 618 tggatgatttttaagttacgtcagaggaatacagcatcgagtcctcaaccctc 677
 Db 819 AGGGGATATTTTGAGCTTAAGAAATGACAGATTTTGTCTGTACAAATGAGCA 878
 QY 678 ctactgattccgagtcagagatgacacacttggggctttaagtctg 728
 Db 879 CTGTATAGACATGACATGAGCCAGCTTTTTCGGGCGCTTTTATGTTGG 929

LT 10
 8-670-354-5
 Sequence 5, Application US/08670354
 Patent No. 5763223
 GENERAL INFORMATION:
 APPLICANT: Steven R. Wiley and
 APPLICANT: Raymond G. Goodwin.
 TITLE OF INVENTION: Cytokine That Induces Apoptosis
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: Apple 7.5.2
 SOFTWARE: Microsoft Word, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/670.354
 FILING DATE: 25-JUN-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/496.632
 FILING DATE: 29-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/548.368
 FILING DATE: 01-NOV-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2835-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1366 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE:
 CLONE: MuAIC
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 47..919

US-08-670-354-5
 Query Match 7.8%; Score 57.6; DB 2; Length 1366;
 Best Local Similarity 49.7%; Pred. No. 3.1e-09;
 Matches 187; Conservative 0; Mismatches 174; Indels 15; Gaps 1.

QY 374 tctcaaatgacttttagcaatggaaaactaatagtttaactgaatggtttattacc 433
 Db 549 TCACACAGGTGCTCTTATGAAATGAGAGCTGTCATGAGAGGAGGCGCTGTATFCA 608
 QY 434 tgtatgcaaacatttgcttgcacatcatgaacttcaggagacta----- 480
 Db 609 TCTATTCCCAACATCATCTTCGATTTCAGGAGCTGAAGACCTTCACAGATGCTCTCA 668
 QY 481 -gctacagagatcttcaactaatggtgtaagtcactcaaaacagcatcaaatccaa 538
 Db 669 AGGACAGGTGAGAACCAACAGCTGTGTCAGTACATCTACAGTACACAGCTATCCGG 728
 QY 539 gtctcataccctgataagagagagacacacagatattgltcaaggaattctgaattcc 598
 Db 729 ATCCCATAGTGTCTCATGAAAGACGCCAGAAACAGCTGTTGGCCAGAGATGCCAGTACG 788
 QY 599 attttatccataacgttggtgatttttaagttacggtctggaagaaatcagca 658
 Db 789 GACTGTACTCATCTATCAGGAGGATTTGCTGACCTAAAAAATGACAGATTTTGG 848
 QY 659 tcgaagttccaaaccccttactggtatccgagtcagagatgacacatacttgggctt 718
 Db 849 TTTCTGTGACAAATGAAATTTGATGAGACTGTGACCTGAAAGAGCGAGCTTTTGSAGCT 908
 QY 719 ttaagttcgagatat 734
 Db 909 TTTTATTAACATAAT 924

RESULT 11
 PCT-US96-10895-5
 Sequence 5, Application PC/TUS9610895
 GENERAL INFORMATION:
 APPLICANT: Immunex Corporation.
 TITLE OF INVENTION: Cytokine That Induces Apoptosis
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: Apple 7.5.2
 SOFTWARE: Microsoft Word, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/10895
 FILING DATE: 25-JUN-1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/496.632
 FILING DATE: 29-JUN-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/548.368
 FILING DATE: 01-NOV-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2835-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MUAIC
FEATURE:
NAME/KEY: CDS
LOCATION: 47...919
PCT-US96-10895-5

Query Match 7.8%; Score 57.6; DB 6; Length 1366;
Best Local Similarity 49.7%; Pred. No. 3.1e-09;
Matches 187; Conservative 0; Mismatches 174; Indels 15; Gaps 1;

QY 374 tctccacatgacttttagcaatggaaaactaatagtaatacaggatgctttattacc 433
DB 549 TCAACCAAGTGTCTTTAGAAATGAGAGCTGTCTATGAGCAGGAGGCGCTGATTTACA 608
QY 434 tctatgcaaacatttgcttgcacatcatgaaacttcaggagacct----- 480
DB 609 TCTATCCCAACATCATCTCCATTTTCAGGAGCTGAAAGACCTCCCAAGATGCTCTCAA 668
QY 481 -ggtaacagagatcttaactaatggtgtactaactaaacacagcatcaaatcccaa 538
DB 669 AGGACAAAGTGAAGCAACAGCTGCTCAGTACATCTACAGATACACACTATCCGG 728
QY 539 gtctcataccctgtaagaaggagacacacagtaattgctcagggaattctgaattcc 598
DB 729 ATCCCATGATGCTCATGAAGAGCGCCAGAAACAGCTGTGTGCCAGATGCCAGTACG 788
QY 599 attttatccctaaagcttggtgatttttaagttacggtcctgagggagaaatcaagaa 658
DB 789 GACTTACTCTCATCTATCAGGAGGATTTGACCTAAATAAATGACAGATTCTTGG 848
QY 659 tcgaaggtctcaaccctctactcgtgacgcgatacgaagtgcacacatacttgggctt 718
DB 849 TTTCTGTGACAAATGAACCTTTTGATGAGCCTGATCAAGAACCAGCTTCTTGAGCCT 908
QY 719 ttaagttcgagatat 734
DB 909 TTTTATTAATACTAAT 924

RESULT 12
US-08-584-031-3
Sequence 3, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 390
TYPE: DNA
ORGANISM: Homo sapiens
US-08-584-031-3

Query Match 5.0%; Score 37.4; DB 5; Length 390;
Best Local Similarity 64.4%; Pred. No. 0.0066;

Matches 56; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 378 caacatgacttttagcaatggaaaactaatagtaatacaggatgctttattaccgta 437
DB 302 caacttgacttgaggatggtgactggtatccatgaaaagggttttactacatcta 361
QY 438 tgcacacattgcttgcacatcatga 464
DB 362 ttcccaaacatcttgcatttcagga 388

RESULT 13
US-08-780-496-3
Sequence 3, Application US/08780496
Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Anan Chuntharapal, Kyung Jin Kim
TITLE OF INVENTION: APO-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-780-496-3

Query Match 5.0%; Score 37.4; DB 5; Length 390;
Best Local Similarity 64.4%; Pred. No. 0.0066;
Matches 56; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 378 caacatgacttttagcaatggaaaactaatagtaatacaggatgctttattaccgta 437
DB 302 CAACTTGACACTTGAGGAATGTTGAACTGTCATCCATGAAAAAGGTTTACTACATCTA 361
QY 438 tgcacacattgcttgcacatcatga 464
DB 362 TTCCCAACATACTTTCGATTTCAGGA 388

RESULT 14
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
APPLICANT: FALKNER, F. G.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2000, 14:55:50 ; Search time 54.03 Seconds
(without alignments)
76.314 Million cell updates/sec

Title: US-09-202-455-17
Perfect score: 1301
Sequence: 1 AQMDPNRISDGTGHCYRII.....LLDPDDATYFGAFKVRDID 246

Scoring table: BLOSUM62
Gapop10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 164575
Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1301	100.0	317	3	US-08-996-139-13
2	1116	85.8	294	4	US-08-996-139-13
3	1109	85.2	316	2	US-08-842-842-7
4	235.5	18.1	281	1	US-08-670-334-2
5	235.5	18.1	281	1	US-08-584-031-1
6	235.5	18.1	281	4	US-08-780-496-1
7	235.5	18.1	281	4	PCT-US96-10895-2
8	235	18.1	291	4	US-08-670-334-6
9	235	18.1	291	4	PCT-US96-10895-6
10	164.5	12.6	376	3	US-08-751-512-8
11	160	12.3	279	4	PCT-US95-00362-5
12	157	12.1	287	3	US-08-815-190A-16
13	150	11.5	261	1	US-07-940-605A-2
14	150	11.5	261	1	US-08-184-422-8
15	150	11.5	261	1	US-08-360-923A-2
16	150	11.5	261	1	US-08-446-922-4
17	150	11.5	261	1	US-08-431-055-4
18	150	11.5	261	2	US-08-690-096-2
19	150	11.5	261	2	US-08-249-189-12
20	150	11.5	261	2	US-08-484-624A-12
21	150	11.5	261	2	US-08-477-733B-12
22	150	11.5	261	3	US-08-763-995-2
23	150	11.5	261	3	US-09-088-913A-12
24	150	11.5	261	3	US-08-589-771B-8
25	150	11.5	261	4	PCT-US93-10034-4
26	150	11.5	273	1	US-08-446-922-11
27	150	11.5	273	2	US-08-249-189-21
28	150	11.5	273	2	US-08-484-624A-21

29	150	11.5	273	2	US-08-477-733B-21	Sequence 21, Appl
30	150	11.5	273	3	US-09-088-913A-21	Sequence 21, Appl
31	150	11.5	473	2	US-08-249-189-16	Sequence 16, Appl
32	150	11.5	473	2	US-08-484-624A-16	Sequence 16, Appl
33	150	11.5	473	2	US-08-477-733B-16	Sequence 16, Appl
34	150	11.5	473	3	US-09-088-913A-16	Sequence 9, Appl
35	149.5	11.5	179	3	US-08-649-100-9	Sequence 9, Appl
36	149.5	11.5	281	2	US-08-810-453-2	Sequence 2, Appl
37	149.5	11.5	281	3	US-08-815-190A-2	Sequence 2, Appl
38	149.5	11.5	281	4	PCT-US95-00362-2	Sequence 2, Appl
39	145.5	11.2	145	3	US-08-630-172-5	Sequence 5, Appl
40	145.5	11.2	378	3	US-08-630-172-21	Sequence 21, Appl
41	141.5	10.9	156	2	US-08-500-860A-36	Sequence 36, Appl
42	141	10.8	155	1	US-07-994-469A-94	Sequence 94, Appl
43	141	10.8	158	1	US-07-794-400-6	Sequence 6, Appl
44	141	10.8	158	1	US-07-994-469A-99	Sequence 99, Appl
45	141	10.8	158	1	US-08-397-470-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-13
Sequence 13, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galbert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-13

102(e)
12-23-97

72-317
11

Query Match 100.0%; Score 1301; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 9.7e-139;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AOMDNRISSEGTGCTIYRLRLHENAADPODTLESODTKLIPDSCRRKQAFQGAOVKEL 60
DB 72 AOMDNRISSEGTGCTIYRLRLHENAADPODTLESODTKLIPDSCRRKQAFQGAOVKEL 131
QY 61 OHIVSGHIRAEKAWVDGSMIDLAKRSKLEAOPFAHLITINATDIPSGSHKVSLSWYHDR 120
DB 132 OHIVSGHIRAEKAWVDGSMIDLAKRSKLEAOPFAHLITINATDIPSGSHKVSLSWYHDR 191
QY 121 GWAKISNMTFSGKLIYNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPS 180
DB 192 GWAKISNMTFSGKLIYNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPS 251
QY 181 SHTLKKGSTKYWGSNFEHFYSINVGGFKLRSGEISIEVSNPLDPPDQATYFGAF 240
DB 252 SHTLKKGSTKYWGSNFEHFYSINVGGFKLRSGEISIEVSNPLDPPDQATYFGAF 311
QY 241 KYRID 246
DB 312 KYRID 317

RESULT 2
US-08-996-139-11
Sequence 11, Application US/08996139
Patent No. 6017729

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-996-139-11
Query Match 85.8%; Score 1116; DB 3; Length 294;
Best Local Similarity 85.0%; Pred. No. 6.7e-118;
Matches 209; Conservative 14; Mismatches 21; Indels 2; Gaps 1;

QY 1 AOMDNRISSEGTGCTIYRLRLHENAADPODTLESODTKLIPDSCRRKQAFQGAOVKEL 60
DB 51 AOMDNRISSEGTGCTIYRLRLHENAADPODTLESODTKLIPDSCRRKQAFQGAOVKEL 108
QY 61 OHIVSGHIRAEKAWVDGSMIDLAKRSKLEAOPFAHLITINATDIPSGSHKVSLSWYHDR 120
DB 109 OHIVSGHIRAEKAWVDGSMIDLAKRSKLEAOPFAHLITINATDIPSGSHKVSLSWYHDR 168
QY 121 GWAKISNMTFSGKLIYNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPS 180
DB 169 GWAKISNMTFSGKLIYNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPS 228
QY 181 SHTLKKGSTKYWGSNFEHFYSINVGGFKLRSGEISIEVSNPLDPPDQATYFGAF 240
DB 229 SHTLKKGSTKYWGSNFEHFYSINVGGFKLRSGEISIEVSNPLDPPDQATYFGAF 288
QY 241 KYRID 246
DB 289 KYRID 294

RESULT 3
US-08-842-842-7
Sequence 7, Application US/08842842
Patent No. 5843678

GENERAL INFORMATION:
APPLICANT: Boye, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA

ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-842-842-7

Query Match 85.2%; Score 1109; DB 2; Length 316;
Best Local Similarity 84.6%; Pred. No. 4.7e-117;
Matches 208; Conservative 14; Mismatches 22; Indels 2; Gaps 1;

QY 1 AOMDNRISSEGTGCTIYRLRLHENAADPODTLESODTKLIPDSCRRKQAFQGAOVKEL 60
DB 73 AOMDNRISSEGTGCTIYRLRLHENAADPODTLESODTKLIPDSCRRKQAFQGAOVKEL 130
QY 61 OHIVSGHIRAEKAWVDGSMIDLAKRSKLEAOPFAHLITINATDIPSGSHKVSLSWYHDR 120

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Db 131 OHVGPORFSCAPAMWESSWLDVAORGPKEAPRAHLITINASPSSGSHKVTLSWYDR 190
QY 121 GWAKISNMTFSGNKLIVNODGFYLLANICFRHHETSGDLATEYLQLMVYTKTSIKIPS 180
Db 191 GWAKISNMTLSNGKLRVQDGFYLLANICFRHHETSGSVPTDYLQLMVYTKTSIKIPS 250
QY 181 SHTLMKGGSTIKYSGNSEFHYSINVGFEKLRSGEISIEVSNPSLDDPDATYFGAF 240
Db 251 SHNLMKGGSTIKYSGNSEFHYSINVGFEKLRSGEISIEVSNPSLDDPDATYFGAF 310
QY 241 KYRDID 246
Db 311 KYRDID 316

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RESULT 4

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US-08-670-354-2
Sequence 2, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670.354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496.632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548.368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-354-2

```

```

Query Match 18.1%; Score 235.5; DB 1; Length 281;
Best Local Similarity 25.3%; Pred. No. 1.7e-18;
Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;
QY 6 NRISDGTGHCIRILRLHENDADPDTLESODTKLIPSCSRIRKQAFGAVQKELOHYG 65
Db 47 DKYSKSGIACF-----LKED---DSYMDPNDDESMNSPCWQVKM-----QLRQLVR 89

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QY 66 SQHIRAKAMVDGSMWLAKRSKLEAQP-----AHLT-----INATDIPSGSHK 110
Db 90 KMLRTSEETI-----STVDEKQONISPLVREGRPQRYAAHITGRGNSNLSPSNKE 144
QY 111 VSL-----SSWYHDR-GWAKISNMTFSGNKLIVNODGFYLLANICFRHHETSGDLATEYL 165
Db 145 KALGRKINSWESSRSGHSFLSNLHLRNGELVYHEKGFYIYSQYFFRQEIKEKNTKNDK 204
QY 166 QLMVYTKTSIKIPSSHTLMKGGSTIKYSGNSEFHYSINVGFEKLRSGEISIEVSNP 225
Db 205 QMVOYIYKYT--SYDPDILMKSARNSCSKDAEYGLYSIYGGLFELKENDRIEVSATNE 263
QY 226 SLDDPDATYFGAFKV 242
Db 264 HLIDMDHEASFFGAFV 280

```

RESULT 5

```

US-08-584-031-1
Sequence 1, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.220S03
CURRENT APPLICATION NUMBER: US/08/584.031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-1

```

```

Query Match 18.1%; Score 235.5; DB 3; Length 281;
Best Local Similarity 25.3%; Pred. No. 1.7e-18;
Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;

```

```

QY 6 NRISDGTGHCIRILRLHENDADPDTLESODTKLIPSCSRIRKQAFGAVQKELOHYG 65
Db 47 DKYSKSGIACF-----LKED---DSYMDPNDDESMNSPCWQVKM-----QLRQLVR 89
QY 66 SQHIRAKAMVDGSMWLAKRSKLEAQP-----AHLT-----INATDIPSGSHK 110
Db 90 KMLRTSEETI-----STVDEKQONISPLVREGRPQRYAAHITGRGNSNLSPSNKE 144
QY 111 VSL-----SSWYHDR-GWAKISNMTFSGNKLIVNODGFYLLANICFRHHETSGDLATEYL 165
Db 145 KALGRKINSWESSRSGHSFLSNLHLRNGELVYHEKGFYIYSQYFFRQEIKEKNTKNDK 204
QY 166 QLMVYTKTSIKIPSSHTLMKGGSTIKYSGNSEFHYSINVGFEKLRSGEISIEVSNP 225
Db 205 QMVOYIYKYT--SYDPDILMKSARNSCSKDAEYGLYSIYGGLFELKENDRIEVSATNE 263
QY 226 SLDDPDATYFGAFKV 242
Db 264 HLIDMDHEASFFGAFV 280

```

```

RESULT 6
US-08-780-496-1
Sequence 1, Application US/08780496
Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd

```

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780.496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maichang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-780-496-1

Query Match 18.1%; Score 235.5; DB 3; Length 281;
Best Local Similarity 25.3%; Pred. No. 1,7e-18;
Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;

QY 6 NRISDGHCHYRILRLHENAFODTTLESODTKLIPDSRRIRKQAFQGAOKELQHYG 65
DB 47 DKYSKGIACF-----LKED-----DSYWDPNDESMNSPCQVW-----QLRQLVR 89
QY 66 SQHIAEAMVDSWLDLAKRSKLEAOPF-----AHLT-----INATDIPSGSK 110
DB 90 KMLTSETT-----STVQEKQONISPLVREGRFORVAHAHITGRGNSNTLSSPNSKNE 144
QY 111 VSL-----SSWYHDR-GWAKISNMTFSGKLIYNODGFYLLYANICFRHHTSGDLATEYL 165
DB 145 KALGRKINSWESSRSGHSLNLHRLNGELVTHEKGFIYISQTYFRQGEIKENTKNDK 204
QY 166 QLMVYVITSTKIPSSHTLMKGGSTKTYSGNSEHFHYSINVGCFKRLSGEISIEVSNP 225
DB 205 QMVOYIYKTYT-SYDPPIILMKARSNCWSKDAEYGLYSIYOGGIFELKENDRIEVSVTNE 263
QY 226 SLDDPDODATYGAFAKV 242
DB 264 HLIDMDHEASFFGAPLV 280

RESULT 7
PCT-US96-10895-2
Sequence 2, Application PC/TUS9610895
GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cyclokin That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match 18.1%; Score 235.5; DB 4; Length 281;
Best Local Similarity 25.3%; Pred. No. 1,7e-18;
Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;

QY 6 NRISDGHCHYRILRLHENAFODTTLESODTKLIPDSRRIRKQAFQGAOKELQHYG 65
DB 47 DKYSKGIACF-----LKED-----DSYWDPNDESMNSPCQVW-----QLRQLVR 89
QY 66 SQHIAEAMVDSWLDLAKRSKLEAOPF-----AHLT-----INATDIPSGSK 110
DB 90 KMLTSETT-----STVQEKQONISPLVREGRFORVAHAHITGRGNSNTLSSPNSKNE 144
QY 111 VSL-----SSWYHDR-GWAKISNMTFSGKLIYNODGFYLLYANICFRHHTSGDLATEYL 165
DB 145 KALGRKINSWESSRSGHSLNLHRLNGELVTHEKGFIYISQTYFRQGEIKENTKNDK 204
QY 166 QLMVYVITSTKIPSSHTLMKGGSTKTYSGNSEHFHYSINVGCFKRLSGEISIEVSNP 225
DB 205 QMVOYIYKTYT-SYDPPIILMKARSNCWSKDAEYGLYSIYOGGIFELKENDRIEVSVTNE 263
QY 226 SLDDPDODATYGAFAKV 242
DB 264 HLIDMDHEASFFGAPLV 280

RESULT 8
US-08-670-354-6
Sequence 6, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cyclokin That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh

```

1      OPERATING SYSTEM: Apple 7.5.2
2      SOFTWARE: Microsoft Word, Version 6.0.1
3      CURRENT APPLICATION DATA:
4      APPLICATION NUMBER: US/08/670,354
5      FILING DATE: 25-JUN-1996
6      CLASSIFICATION: 435
7      PRIOR APPLICATION DATA:
8      APPLICATION NUMBER: US 08/496,632
9      FILING DATE: 29-JUN-1995
10     CLASSIFICATION: 435
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER: US 08/548,368
13     FILING DATE: 01-NOV-1995
14     CLASSIFICATION: 435
15     ATTORNEY/AGENT INFORMATION:
16     NAME: Anderson, Kathryn A.
17     REGISTRATION NUMBER: 32,172
18     REFERENCE/DOCKET NUMBER: 2835-B
19     TELECOMMUNICATION INFORMATION:
20     TELEPHONE: (206) 587-0430
21     TELEFAX: (206) 233-0644
22     TELEX: 756822
23     INFORMATION FOR SEQ ID NO: 6:
24     SEQUENCE CHARACTERISTICS:
25     LENGTH: 291 amino acids
26     TYPE: amino acid
27     TOPOLOGY: linear
28     MOLECULE TYPE: protein
29     US-08-670-354-6

```

Query Match	18.1%	Score 235;	DB 1;	Length 291;
Best Local Similarity	25.6%	Pred. No. 2.1e-18;		
Matches 72;	Conservative 47;	Mismatches 84;	Indels 78;	Gaps 12

```

QY 2 QMDNRRISDESDTHOYIRLRLRHEMADODPTLESQDPKRLPDSORRLK-----49
Db 48 QLODN-YKIGLAFSK-----TDEDWDS-----DEILNRPLOQYKRQLOLYOIEVTL 97
QY 50 QAFQ-----GAVQKELOHVGSCHIRAKMAYDGSWMLDAKRSKLE 90
Db 98 RTFODITSTYPERKOLSTPEPLRGGRPKVAHNGITR-KSNSALI-----PIKDGKTL 151
QY 91 AOPFHLINNTDIPSGSHKXJLSWYHNR-GMKKINMPTNSCKLIVNODGFYLVANI 159
Db 152 GQ-----KISWESSRKGHSFLNHLVLRNSELVTEODGLYITYSQT 192
QY 150 CFRHHETSGDATEYL-----OLMWYVYKTSIKIPSSHLLKSGSTXWGSNBEHF 201
Db 193 YERFQEAED-ASKWVSKDKVYRQOLVQYIKYKT-SYPDPYLVLMKKSARNCSMDPAEYL 249
QY 202 YSINVGFFKLRSGBEISIEVNSLLDDPDDADYFFCAFXY 242
Db 250 YSIIYGGFLELKNDRFVSYVNTHEMLMDODEASFFGFGLI 290

```

RESULT 9
 PCT-US96-10895-6
 : Sequence 6, Application PC/TUS9610895
 : GENERAL INFORMATION:
 : APPLICANT: Immunex Corporation.
 : TITLE OF INVENTION: Cytokine That Induces Apoptosis
 : NUMBER OF SEQUENCES: 9
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Kathryn A. Anderson, Immunex Corporation
 : STREET: 51 University Street
 : CITY: Seattle
 : STATE: WA
 : COUNTRY: USA
 : ZIP: 98101
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: Apple Macintosh

```

1      OPERATING SYSTEM: Apple 7.5.2
2      SOFTWARE: Microsoft Word, Version 6.0.1
3
4      CURRENT APPLICATION DATA:
5      : APPLICATION NUMBER: PCT/US96/10895
6      : FILING DATE: 25-JUN-1996
7      CLASSIFICATION:
8
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER: US 08/496,632
11     FILING DATE: 29-JUN-1995
12     CLASSIFICATION:
13     PRIOR APPLICATION DATA:
14     APPLICATION NUMBER:
15     FILING DATE: 01-NOV-1995
16     CLASSIFICATION:
17
18     ATTORNEY/AGENT INFORMATION:
19     NAME: Anderson, Kathryn A.
20     REGISTRATION NUMBER: 32,172
21     REFERENCE/DOCKET NUMBER: 2835-WO
22     TELECOMMUNICATION INFORMATION:
23     TELEPHONE: (206) 587-0430
24     TELEFAX: (206) 233-0644
25     TELEX: 756822
26
27     INFORMATION FOR SEQ ID NO: 6:
28     SEQUENCE CHARACTERISTICS:
29     LENGTH: 291 amino acids
30     TYPE: amino acid
31     TOPOLOGY: linear
32     MOLECULE TYPE: protein
33
34     PCT-US96-10895-6
35
36     I

```

Query Match	18.1%;	Score	235;	DB	4;	Length	291;
Best Local Similarity	25.6%;	Pred. No.	2.1e-18;				
Matches	72;	Conservative	47;	Mismatches	84;	Indels	78;
						Gaps	12;

```

QY      2 QMDPNRISSEDTHTYRLRLRLEHMAEDPDTLIESDPTKLPPDSORRRTK-----49
Db      48 QLOQDN-YSKIPLAFSK-----TDEDWDSD-----DDEILNRPLOLYKRLQLOYLEVTL 97
QY      50 QAFQ-----GAVQKELOHTYVSGCHIRAEKAMVDGSWLDLAKNSKLE 90
Db      98 RTFDOTLSTVPEKOLSTPPLEPRGGRPQKVAHITGILR-RSNSALI-----PISKDEKTL 150
QY      91 AQPFAHLTINNTDLPSCGHKXKLSLWYHNR-GMKKISMFMNSCKLLVNDGGFYLVANI 149
Db      152 GQ-----KIESWESSKRGHSEFLNHVLEFRNGELVITEODGYYIYTSQT 192
QY      150 CFRHHTSGD.LATEYL-----QLMWYVYKTSIKIPSSHTLMKSGSTRYWGNSSEFHF 201
Db      193 YFRFQEAED--ASKWVSKDKVRYKQLOLYIKYRT-SYDPDLYLTKSRANSQMSRDAEYGL 249
QY      202 YSINVGSEFFKLRSGEETISIEVNSLDDPDDADYPAFAFY 242
Db      230 YSIYGGLEFLTKKNDRI.FVSYTNLHLDLDDDEASFEGFGL 290

```

US-08-751-512-8
Sequence 8, Application US/08751512
Patent No. 6001962
GENERAL INFORMATION:
APPLICANT: Ramar, J. Kevin
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: Modified FMS Ligands
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,512
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Matthew B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 02307K-07100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
8-751-512-8

Query Match 12.6%; Score 164.5; DB 3; Length 376;
Best Local Similarity 23.6%; Pred. No. 2.8e-10;
Matches 59; Conservative 39; Mismatches 89; Indels 63; Gaps 9;

QY 32 TLESODTKIPSCRIRKAFQAGV-----QKELQIVSQ--HRAEKA 74
DB 151 TIASOPLSLRPACR--PAGGAVHTRGLDPALEHHHHHEFEFMPQDLHOKELA 207
QY 75 MYDGSWDLAKRSKLEAQ-----PFAHLT--INATDIPSGSHKVSLSMYH 118
DB 208 ELRETSQMHNTASSLEKQIGHPSPEPEKELKVAHLTKSNRSP-----LEWED 259
QY 119 DRGMAKISNMTFSNGKLIYNODGFYLYANICFRHHTSGDLATEYLQMLVYTKTSIKI 178
DB 260 TYGIYLSGVKKYKKGGLVNETGLVFYSKYVFRGQSCNN-----LPLSHKYVMNSKY 313
QY 179 PSSHTLMKGGSTKY-----WGSNFEHFYSINVGFFLRGSELSIEVSNPSLDPQ 232
DB 314 PDOLVMECKMNSYCTGTGMWARRS-----YLGAVFILTADHLVYSELCLVNEBE 366
QY 233 DATYFAGKRV 242
DB 367 SOTFFGLYKL 376

US95-00362-5
Sequence 5, Application PC/TUS9500362
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: Ligand That Binds Fas Antigen
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00362
FILING DATE: 06-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/179,138
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,559
FILING DATE: 01-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2805-WO
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00362-5

Query Match 12.3%; Score 160; DB 4; Length 279;
Best Local Similarity 25.9%; Pred. No. 5.7e-10;
Matches 50; Conservative 39; Mismatches 80; Indels 24; Gaps 8;

QY 56 VOKELQHT--VGSQHTRA---EKANVDSWDLAKRSKLEQPFRAHLTINATDIPSGSHK 110
DB 105 LQKELAELEERTNOSLKVSSEKQIANPS---TPSEKKEPRVAHLTGN-----PHS 153
QY 111 VSLT-SWYHDGMAKISNMTFSNGKLIYNODGFYLYANICFRHHTSGDLATEYLQMLV 169
DB 154 RSIPLMEDTYGTALISGVKKYKKGGLVNETGLVFYSKYVFRGQSCN---NOLNKHV 209
QY 170 YTKTSIKRIPSHHTLMKGGSTKYWGSNFEHFYSINVGFFLRGSELSIEVSNPSLDD 229
DB 210 YMRNS--KYPDVLVMECKRLNLYFR--TGQIWAHSYLGAVFNLTSADHLVYNISQLSLIN 266
QY 230 PDQATYFAGKRV 242
DB 267 FEESKTFGLYKL 279

RESULT 12
US-08-815-190A-16
Sequence 16, Application US/08815190A
Patent No. 6046310
GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,190A
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,584
FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 011823-0067100US

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? TELECOMMUNICATIONS INFORMATION
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 16:
? SEQUENCE CHARACTERISTICS:
?   LENGTH: 287 amino acids
?   TYPE: amino acid
?   TOPOLOGY: linear
?   MOLECULE TYPE: protein
?
US-08-815-190A-16

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Query Match	12.1%	Score 157	DB 3:	Length 287
Best Local Similarity	23.0%	Pred	No. 1.3e-09	
Matches	61	Conservative	42	Mismatches 104; Indels 58; Gaps 10

[illegible]

RESULT 13
 US-07-940-605A-2
 Sequence 2, Application US/07940605A
 Patent No. 5540926
 GENERAL INFORMATION:
 APPLICANT: ARUFFO, ALEJANDRO
 APPLICANT: HOLLENAUGH, DIANE
 APPLICANT: LEDBETTER, JEFFREY A.
 TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.255A
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/940,605A
 FILING DATE: 04-SEP-1992
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 562A-184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS: 2

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; LENGTH: 261 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-07-940-605A-2

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Query Match	11.5%	Score 150;	DB 1;	Length 261;
Best Local Similarity	25.4%;	Pred. No. 6.8e-09;		
Matches	58;	Conservative	43;	Mismatches 95;
			Indels	32;
			Gaps	12

[illegible]

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MOLECULE TYPE: protein
US-08-184-422-8

Query Match 11.5%; Score 150; DB 1; Length 261;
Best Local Similarity 25.4%; Pred. No. 6.8e-09;
Matches 58; Conservative 43; Mismatches 95; Indels 32; Gaps 12;

QY 22 LHENDFQDT--TLESQDTKLIPDSCRRIKQAFQAVQKELQIHVGSQHIRAKNVDGS 79
DB 59 LHEDVFPMKTIQRCNTGERSLSLNCCEIKSQEGFV-KDIM-----LNKEETKENS 110
QY 80 WDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSWYHDGMAKISN--MTFSNGK-LI 136
DB 111 F-EMQKGDQ-NPQIAHAVISEAS-----SKTTSVLQW-AEKGYTMSNNLVTLENGKQLT 162
QY 137 VNODGFYLYIANICFRHHETSGDLATEYLQIMVYVTKTSIKIPS--SHTLMKGSTKYWS 194
DB 163 YKRGGLYIYIAQVTFCSNREASSQAP-----FIASLCLKSPGRFERILLRANTH--S 213
195 GNSEPHFYISINVGFFKLRSGEISIEVSNPSLDDPDQDATYFGAKV 242
214 SAKPCGQOSIHGQVFELOPGASVFNVTDPQSVSHGTGFTSFGLLKL 261

RESULT 15
US-08-360-923A-2
Sequence 2, Application US/08360923A

Patent No. 5674492

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: LONGO, DAN L.

APPLICANT: MORPHY, WILLIAM

TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING

TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS

TITLE OF INVENTION: EXPRESSING CD40

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: Apple Macintosh System 7.1

SOFTWARE: Microsoft Word for Macintosh, Version #5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,923A

FILING DATE: December 21, 1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/172,664

FILING DATE: December 23, 1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2818-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-360-923A-2

Query Match 11.5%; Score 150; DB 1; Length 261;
Best Local Similarity 25.4%; Pred. No. 6.8e-09;
Matches 58; Conservative 43; Mismatches 95; Indels 32; Gaps 12;

QY 22 LHENDFQDT--TLESQDTKLIPDSCRRIKQAFQAVQKELQIHVGSQHIRAKNVDGS 79
DB 59 LHEDVFPMKTIQRCNTGERSLSLNCCEIKSQEGFV-KDIM-----LNKEETKENS 110
QY 80 WDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSWYHDGMAKISN--MTFSNGK-LI 136
DB 111 F-EMQKGDQ-NPQIAHAVISEAS-----SKTTSVLQW-AEKGYTMSNNLVTLENGKQLT 162
QY 137 VNODGFYLYIANICFRHHETSGDLATEYLQIMVYVTKTSIKIPS--SHTLMKGSTKYWS 194
DB 163 YKRGGLYIYIAQVTFCSNREASSQAP-----FIASLCLKSPGRFERILLRANTH--S 213
195 GNSEPHFYISINVGFFKLRSGEISIEVSNPSLDDPDQDATYFGAKV 242
214 SAKPCGQOSIHGQVFELOPGASVFNVTDPQSVSHGTGFTSFGLLKL 261

Search completed: November 1, 2000, 17:58:49
Job time: 10979 sec

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